

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 7, 2006, 23:30:34 ; Search time 17.6033 Seconds
(without alignments)
1864.554 Million cell updates/sec

Title: US-10-621-855-5
Perfect score: 2131
Sequence: 1 MGLSWSPRPPLMLLLVLS.....PRLPILSFLPILLQLTLW 397

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pap.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pap.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pap.*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pap.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2131	100.0	397	2	US-09-220-528-64
2	2131	100.0	397	2	US-09-187-906-17
3	2131	100.0	397	2	US-09-489-407-17
4	1774	83.2	346	2	US-09-187-906-15
5	1774	83.2	346	2	US-09-489-407-15
6	1646.5	77.3	400	2	US-09-220-528-63
7	1646.5	77.3	400	2	US-09-187-906-21
8	1646.5	77.3	400	2	US-09-949-016-9079
9	1646.5	77.3	400	2	US-09-489-407-21
10	1386	65.0	315	2	US-09-187-906-19
11	1386	65.0	315	2	US-09-489-407-19
12	577.5	27.1	445	2	US-08-861-990-11
13	577.5	27.1	464	2	US-08-957-063-6
14	577.5	27.1	464	2	US-09-487-685-6
15	577.5	27.1	464	2	US-08-802-805D-6
16	577.5	27.1	464	2	US-08-861-990-2
17	577.5	27.1	464	2	US-08-388-316C-6
18	577.5	27.1	664	2	US-08-957-063-18
19	577.5	27.1	664	2	US-09-487-685-18
20	577.5	27.1	664	2	US-08-802-805D-18
21	577.5	27.1	664	2	US-09-388-316C-18
22	574.5	27.0	464	2	US-08-957-063-3
23	574.5	27.0	464	2	US-08-487-685-3
24	574.5	27.0	464	2	US-08-802-805D-3
25	574.5	27.0	464	2	US-09-187-906-13
26	574.5	27.0	464	2	US-08-861-990-9
27	574.5	27.0	464	2	US-09-388-316C-3

28	574.5	27.0	464	2	US-09-489-407-13	Sequence 13, Appl
29	574.5	27.0	664	2	US-08-957-063-16	Sequence 16, Appl
30	574.5	27.0	664	2	US-09-487-685-16	Sequence 16, Appl
31	574.5	27.0	664	2	US-08-802-805D-16	Sequence 16, Appl
32	574.5	27.0	664	2	US-09-388-316C-16	Sequence 16, Appl
33	515	24.2	460	2	US-08-802-805D-22	Sequence 22, Appl
34	515	24.2	460	2	US-09-187-906-11	Sequence 11, Appl
35	515	24.2	460	2	US-09-489-407-11	Sequence 11, Appl
36	513.5	24.1	463	2	US-08-837-199A-10	Sequence 10, Appl
37	513.5	24.1	463	2	US-08-837-199A-12	Sequence 12, Appl
38	513.5	24.1	465	2	US-08-837-199A-2	Sequence 2, Appl
39	513.5	24.1	465	2	US-08-861-990-8	Sequence 8, Appl
40	513.5	24.1	465	2	US-09-388-316C-22	Sequence 22, Appl
41	512.5	24.0	465	2	US-08-837-199A-6	Sequence 6, Appl
42	505.5	23.7	468	2	US-08-802-805D-21	Sequence 21, Appl
43	505.5	23.7	468	2	US-08-837-199A-4	Sequence 4, Appl
44	505.5	23.7	468	2	US-08-860-370-2	Sequence 2, Appl
45	505.5	23.7	468	2	US-09-187-906-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-220-528-64
; Sequence 64, Application US/09220528A
; Patent No. 6284540
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
; APPLICANT: Baloh, Robert H.
; TITLE OF INVENTION: Artemin, A No. 6284540e1 Neurotrophic Factor
; FILE REFERENCE: 6029-7998
; CURRENT APPLICATION NUMBER: US/09/220,528A
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: 09/218,698
; EARLIER FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/108,148
; EARLIER FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: 09/163,283
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: Patent in ver. 2.0
; SEQ ID NO 64
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Murine
US-09-220-528-64

Query Match	100.0%	Score 2131;	DB 2;	Length 397;
Best Local Similarity	100.0%	Pred. No. 2.2e-211;		
Matches 397;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MGLSWSPRPPLMLLLVLSLWPLGAGNSLATERNFVNSCTQARKKEANPACKAAAYQH	60	
Db	1	MGLSWSPRPPLMLLLVLSLWPLGAGNSLATERNFVNSCTQARKKEANPACKAAAYQH	60	
Qy	61	LGSCSTLSRPLPLEESAMSDCLEAEQRLNSSLIDCRHRRMKHQATCLDIYTVTHPA	120	
Db	61	LGSCSTLSRPLPLEESAMSDCLEAEQRLNSSLIDCRHRRMKHQATCLDIYTVTHPA	120	
Qy	121	RLSGDYELDVSPYEDVTTSKPKMNLKLNKLKLPDSCLCLFAMLCTLHDKCDRLRKAYG	180	
Db	121	RLSGDYELDVSPYEDVTTSKPKMNLKLNKLKLPDSCLCLFAMLCTLHDKCDRLRKAYG	180	
Qy	181	EACSGIRCOHRLCIAQLRSFFKAAESHAQGLLPCAPEDAGCGERRNTIAPSCALPS	240	
Db	181	EACSGIRCOHRLCIAQLRSFFKAAESHAQGLLPCAPEDAGCGERRNTIAPSCALPS	240	
Qy	241	VTNCLDLRSFCRADPLCRSLMDFOFTHCHPMIDLGTTCATEQSLRAYLGLICTAMTPN	300	
Db	241	VTNCLDLRSFCRADPLCRSLMDFOFTHCHPMIDLGTTCATEQSLRAYLGLICTAMTPN	300	
Qy	301	FISKVNTTVALSCTCRSGNLQDECEQLERSFSQNPCLVEIAAKMRFRHLQFSQDWADS	360	

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Db      301 FISKVNTTVALSCTCRGSGNLDQECQLRSFSQNPCLVEAIAAKMRPHRQLFSQDWADS 360
QY      361 TFSVVQQNSNPALRLQPLRPILSFSILPLILLQTLW 397
Db      361 TFSVVQQNSNPALRLQPLRPILSFSILPLILLQTLW 397

RESULT 2
US-09-187-906-17
; Sequence 17, Application US/09187906
; Patent No. 6627135
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/187,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2838
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-187-906-17

Query Match 100.0%; Score 2131; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.2e-211;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MGLSWSPRPLMLILLVLSLPLCGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60
Db      1 MGLSWSPRPLMLILLVLSLPLCGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60
QY      61 LGSCTSSLSRPLPESAMSADCLEAAEQLRNSSLIDCRRMKHQATCLDIYTWVHPA 120
Db      61 LGSCTSSLSRPLPESAMSADCLEAAEQLRNSSLIDCRRMKHQATCLDIYTWVHPA 120

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QY      121 RSLGDIYELDVSPYEDTVTSKPKWMNLSKLNMLKPSDILCLKPFAMLCCTLHDKCDRLRKAYG 180
Db      121 RSLGDIYELDVSPYEDTVTSKPKWMNLSKLNMLKPSDILCLKPFAMLCCTLHDKCDRLRKAYG 180
QY      181 EACSGIRCORHLCLAQLRSFFFEKAAESHAQGLLLCCPCAPEDAGCGERRNTIAPSCALPS 240
Db      181 EACSGIRCORHLCLAQLRSFFFEKAAESHAQGLLLCCPCAPEDAGCGERRNTIAPSCALPS 240
QY      241 VTPNCLDLRSFCRADPLCRSLRMLDFQTHCHPMDIILGTCAEQSRCLRAYLGLIGTAMTPN 300
Db      241 VTPNCLDLRSFCRADPLCRSLRMLDFQTHCHPMDIILGTCAEQSRCLRAYLGLIGTAMTPN 300
QY      301 FISKVNTTVALSCTCRGSGNLDQECQLRSFSQNPCLVEAIAAKMRPHRQLFSQDWADS 360
Db      301 FISKVNTTVALSCTCRGSGNLDQECQLRSFSQNPCLVEAIAAKMRPHRQLFSQDWADS 360
QY      361 TFSVVQQNSNPALRLQPLRPILSFSILPLILLQTLW 397
Db      361 TFSVVQQNSNPALRLQPLRPILSFSILPLILLQTLW 397

RESULT 3
US-09-489-407-17
; Sequence 17, Application US/09489407
; Patent No. 6861509
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/489,407
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2838
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
US-09-489-407-17

Query Match      100.0%; Score: 2131; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.2e-211; Indels 0; Gaps 0;
Matches 397; Conservative 0; Mismatches 0;

Qy 1 MGLSWSPRPPLMLLLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYQH 60
Db 1 MGLSWSPRPPLMLLLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYQH 60

Qy 61 LGSCTSSLSRPLPLEESAMSDCLEAAEQLRNSLIDCRCHRRMKHQATCLDIYVTHVPA 120
Db 61 LGSCTSSLSRPLPLEESAMSDCLEAAEQLRNSLIDCRCHRRMKHQATCLDIYVTHVPA 120

Qy 121 RSLGDEYLDVSPYEDTVTSKPKWKNLSKLNMLKPDSDCLCKFAMLTCLHDKCDRLRKAYG 180
Db 121 RSLGDEYLDVSPYEDTVTSKPKWKNLSKLNMLKPDSDCLCKFAMLTCLHDKCDRLRKAYG 180

Qy 181 EACSGIRCORHLCLAQLRSFPEKAESAHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240
Db 181 EACSGIRCORHLCLAQLRSFPEKAESAHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240

Qy 241 VTPNCLDLRSTCRADPLCRSLMDPQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPN 300
Db 241 VTPNCLDLRSTCRADPLCRSLMDPQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPN 300

Qy 301 FISKVNTTVALSCTCRSGNLODCEQLERSFSONPCIVEAIAAKMRPHROLFSQDWADS 360
Db 301 FISKVNTTVALSCTCRSGNLODCEQLERSFSONPCIVEAIAAKMRPHROLFSQDWADS 360

Qy 361 TFSVVQQNSNPALRLOPRLPILSILPILLIQLTLW 397
Db 361 TFSVVQQNSNPALRLOPRLPILSILPILLIQLTLW 397

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RESULT 4

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US-09-187-906-15
; Sequence 15, Application US/09187906
; Patent No. 6677135
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/187,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-187-906-15

Query Match      83.2%; Score 1774; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.3e-174;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 LSRPLPLEESAMSDCLEAAEQLRNSLIDCRCHRRMKHQATCLDIYVTHVPA 127
Db 17 LSRPLPLEESAMSDCLEAAEQLRNSLIDCRCHRRMKHQATCLDIYVTHVPA 127

Qy 128 LDVSPYEDTVTSKPKWKNLSKLNMLKPDSDCLCKFAMLTCLHDKCDRLRKAYGACSGIR 187
Db 77 LDVSPYEDTVTSKPKWKNLSKLNMLKPDSDCLCKFAMLTCLHDKCDRLRKAYGACSGIR 136

Qy 188 CORHLCLAQLRSFPEKAESAHAQGLLLCPAPEDAGCGERRNTIAPSCALPSVTPNCLD 247
Db 137 CORHLCLAQLRSFPEKAESAHAQGLLLCPAPEDAGCGERRNTIAPSCALPSVTPNCLD 196

Qy 248 LRSFCRADPLCRSLMDPQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNISKVNT 307
Db 197 LRSFCRADPLCRSLMDPQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNISKVNT 256

Qy 308 TVALSCTCRSGNLODCEQLERSFSONPCIVEAIAAKMRPHROLFSQDWADSFVVQQ 367
Db 257 TVALSCTCRSGNLODCEQLERSFSONPCIVEAIAAKMRPHROLFSQDWADSFVVQQ 316

Qy 368 QNSNPALRLOPRLPILSILPILLIQLTLW 397
Db 317 QNSNPALRLOPRLPILSILPILLIQLTLW 346

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RESULT 5

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US-09-489-407-15
; Sequence 15, Application US/09489407
; Patent No. 6861509
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/489,407
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726

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; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-489-407-15

Query Match 83.2%; Score 1774; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.3e-174;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 LSRPLPLESAMSADCLAEAEOLRNSLIDCRCHRMKHOATCLDIYTVHPARSLGDIY 127
Db 17 LSRPLPLESAMSADCLAEAEOLRNSLIDCRCHRMKHOATCLDIYTVHPARSLGDIY 76
QY 128 LDVSPYEDTVTSKPKWKNLSKLNMLKPDSDCLCFAMLCTLDKCDRLRKAYGEACSGIR 187
Db 77 LDVSPYEDTVTSKPKWKNLSKLNMLKPDSDCLCFAMLCTLDKCDRLRKAYGEACSGIR 136
QY 188 CORHCLAQLRSEFFFEKAAESHAQGLLLCPAPEDAGCGERRRNTIAPSCALPSVTPNCID 247
Db 137 CORHCLAQLRSEFFFEKAAESHAQGLLLCPAPEDAGCGERRRNTIAPSCALPSVTPNCID 196
QY 248 LRSFCRADPLCRSLRMDFOTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFISKV 307
Db 197 LRSFCRADPLCRSLRMDFOTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFISKV 256
QY 308 TVALSCTCGSNLQDECEQLERSFSONPCLVEAIAAKMRFHRLQFSQDWDSTFSVQQ 367
Db 257 TVALSCTCGSNLQDECEQLERSFSONPCLVEAIAAKMRFHRLQFSQDWDSTFSVQQ 316
QY 368 QNSNPALRLOPLRPLPILSILPLILLIQTLM 397
Db 317 QNSNPALRLOPLRPLPILSILPLILLIQTLM 346

RESULT 6
US-09-528-528-63
; Sequence 63, Application US/09220528A
; Patent No. 6284540
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
; APPLICANT: Baloh, Robert H.
; TITLE OF INVENTION: Artemin, A No. 6284540e1 Neurotrophic Factor
; FILE REFERENCE: 6029-7998
; CURRENT APPLICATION NUMBER: US/09/220,528A
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: 09/218,698
; EARLIER FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/108,148
; EARLIER FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: 09/163,283
; EARLIER FILING DATE: 1998-09-29

; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-220-528-63

Query Match 77.3%; Score 1646.5; DB 2; Length 400;
Best Local Similarity 77.8%; Pred. No. 2.4e-161;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

QY 7 PRPP-LLMILLVLVSLWPLGAGNSLATENFVNSCTQARKKCEANPACKAAYQHLGSGCT 65
Db 9 PLPPVVLMLLLPLPSPPLAAGDPLPTESRLMNSCLQARRKQADPTCSAAHHLDSDCT 68
QY 66 SSLSRPLPLESAMSADCLAEAEOLRNSLIDCRCHRMKHOATCLDIYTVHPARSLGDI 125
Db 69 SSISTPLSEPSVPADCLAEAOQLRNSLIDCRCHRMKHOATCLDIYTVHPARSLGDI 128
QY 126 YELDVSPYEDTVTSKPKWKNLSKLNMLKPDSDCLCFAMLCTLDKCDRLRKAYGEACSG 185
Db 129 YELDVSPYEDTVTSKPKWKNLSKLNMLKPDSDCLCFAMLCTLDKCDRLRKAYGEACSG 188
QY 186 IRCORHCLAQLRSEFFFEKAAESHAQGLLLCPAPEDAGCGERRRNTIAPSCALPSVTPNC 245
Db 189 PHCQRHVCLRLQTLTFFFEKAAESHAQGLLLCPAPEDAGCGERRRNTIAPSCALPSVTPNC 248
QY 246 LDLRSFCRADPLCRSLRMDFOTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFISKV 305
Db 249 LELRLCFSDPLCRSLRMDFOTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFVSNV 308
QY 306 NTVALSCTCGSNLQDECEQLERSFSONPCLVEAIAAKMRFHRLQFSQDWDSTFSVQQ 365
Db 309 NTVALSCTCGSNLQDECEQLERSFSONPCLVEAIAAKMRFHRLQFSQDWDSTFSVQQ 368
QY 366 QQNSNPALRLOPLRPLPILSILPLILLIQTLM 397
Db 369 AHQENPAVRPQPVPSLFSCTPLILLIQTLM 400

RESULT 7
US-09-187-906-21
; Sequence 21, Application US/09187906
; Patent No. 6677135
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/187,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 7, 2006, 23:29:17 ; Search time 67.6336 Seconds
(without alignments)
2579.093 Million cell updates/sec

Title: US-10-621-855-5
Perfect score: 2131
Sequence: 1 MGLSWSPRPPLMLILLVLS.....PRLPILSFLPILLQLTLW 397

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_21.*
- 1: geneseqp1980s.*
 - 2: geneseqp1990s.*
 - 3: geneseqp2000s.*
 - 4: geneseqp2001s.*
 - 5: geneseqp2002s.*
 - 6: geneseqp2003as.*
 - 7: geneseqp2003bs.*
 - 8: geneseqp2004s.*
 - 9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2131	100.0	397	2	Aaw37461
2	2131	100.0	397	3	Aay84591 Amino aci
3	2131	100.0	397	3	Aay15174 Murine GF
4	2131	100.0	397	8	Adj58709 Murine re
5	2131	100.0	397	9	Adj53845 Mouse ret
6	2131	100.0	397	9	Adz00209 Mouse Ret
7	1972	92.5	397	2	Aaw84182 A GDNFR-a
8	1880	88.2	397	2	Aay15182 GD-GFRalp
9	1774	83.2	346	2	Aaw37465 Mouse Ret
10	1774	83.2	346	8	Adj58707 Murine re
11	1774	83.2	346	9	Adj53843 Partial m
12	1774	83.2	346	9	Adz00207 Mouse Ret
13	1646.5	77.3	400	2	Aaw65116 Human GDN
14	1646.5	77.3	400	2	Aaw37463 Human Ret
15	1646.5	77.3	400	2	Aaw84186 Glial cel
16	1646.5	77.3	400	3	Aay83226 PRO538 Po
17	1646.5	77.3	400	3	Aay84590 Amino aci
18	1646.5	77.3	400	3	Aay15177 Human GFR
19	1646.5	77.3	400	3	AAB19582 Human PRO
20	1646.5	77.3	400	3	AAB24411 Human PRO
21	1646.5	77.3	400	3	AAB00171 PRO538 po
22	1646.5	77.3	400	3	AAB24050 Human PRO
23	1646.5	77.3	400	8	Adj58713 Human ret
24	1646.5	77.3	400	8	Adt94302 Human PRO

25	1646.5	77.3	400	9	ADY53849 Human ret
26	1646.5	77.3	400	9	ADZ00213 Human Ret
27	1646.5	77.3	628	3	Aay15179 GFRalpha3
28	1642.5	77.1	400	2	Aaw84180 A GDNFR-a
29	1640.5	77.0	400	2	Aaw65117 Human GDN
30	1531.5	71.9	378	2	AAW84185 Glial cel
31	1458	68.4	369	3	AAy15178 Human GFR
32	1458	68.4	369	3	AAB19583 Human PRO
33	1458	68.4	369	3	AAB24051 Human PRO
34	1413	66.3	366	9	AEA39229 GRAL-rela
35	1386	65.0	315	2	Aaw37462 Human Ret
36	1386	65.0	315	8	ADJ58711 Human ret
37	1386	65.0	315	9	ADY53847 Partial h
38	1386	65.0	315	9	ADZ00211 Human Ret
39	722	33.9	172	2	AAW65118 Human GDN
40	654	30.7	498	2	Aaw84183 Consensus
41	640.5	30.1	489	2	AAW84298 Consensus
42	577.5	27.1	460	2	AAW84181 A GDNFR-a
43	577.5	27.1	464	2	AAW71602 Rat neut
44	577.5	27.1	464	2	AAW92299 Rat GDNFR
45	577.5	27.1	464	3	AAy80122 Rat neut

ALIGNMENTS

RESULT 1
AAW37461
ID AAW37461 standard; protein; 397 AA.
XX
XX AAW37461;
AC
DT 21-MAY-1998 (first entry)
DE Mouse Ret ligand RetL3.
XX

Ret ligand; RetL3; receptor; signal transduction; mouse;
cell growth; renal cell; nerve cell; renal failure; nephritis;
kidney transplant; toxic injury; hypoxic injury; neurodegeneration;
motor neurone disease; multiple sclerosis; infection; meningitis;
myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury;
spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease;
muscular dystrophy; myasthenia gravis; tumour; therapy.
Mus-musculus.
XX OS
XX
XX WO9744356-A2.
XX
XX 27-NOV-1997.
XX
XX 07-MAY-1997; 97MO-US007726.
XX
XX 08-MAY-1996; 96US-0017427P.
XX 07-JUN-1996; 96US-0019300P.
XX 16-JUL-1996; 96US-0021859P.
XX 11-APR-1997; 97US-0043533P.
XX (BIOJ) BIOGEN INC.
XX
XX Sanicola-Nadel M, Hession C, Cate RL;
XX WPI; 1998-018431/02.
XX N-PSDB; AAV00249.
XX
XX New nucleic acid encoding ret receptor ligands and related proteins -
XX vectors, transformed cells and antibodies, used for promoting cell growth
XX and improving survival of injured cells, especially renal or nerve cells.
XX Claim 2; Page 77-78; 113pp; English.
XX
XX This amino acid sequence comprises mouse Ret ligand (RetL) RetL3, deduced
XX from cDNA clones (see AAV00249) isolated from an EST database and by
XX 5'RACE. Rat and human RetL1, human RetL2 and RetL3 sequences (see

CC AA037457-60 and AA037462-63) are also claimed. RetL is a key component of
CC the Ret signalling pathway that specifically interacts with Ret receptor
CC protein, triggering Ret dimerisation and/or autophosphorylation of the
CC Ret tyrosine kinase domain. Vectors containing retL3 DNA and prokaryotic
CC or eukaryotic host cells transformed or transfected with these vectors
CC are claimed, as well as a method for production of RetL3, its soluble
CC variants and fusion proteins with a toxin, imageable compound or
CC radionuclide. RetL3, optionally when expressed from vectors in vivo, is
CC used to promote growth of new tissue and survival of damaged tissue,
CC particularly kidney or neural tissue. Typical applications are in renal
CC failure, nephritis, kidney transplants, toxic or hypoxic injury,
CC neurodegeneration, motor neurone disease, multiple sclerosis, bacterial,
CC viral or prion infections (e.g. meningitis, myelopathy associated with
CC HIV or Creutzfeldt-Jakob disease), cranial nerve or spinal cord injury,
CC developmental disorders such as Down's syndrome and cerebral palsy, or
CC conditions involving the peripheral nervous system (Lyme disease,
CC muscular dystrophy and myasthenia gravis). Fusion proteins are used to
CC deliver toxins etc. to Ret-expressing cells, especially tumours
XX
XX Sequence 397 AA;

Query Match 100.0%; Score 2131; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 3.5e-198;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSWSPRPPLMLILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYQH 60
Db 1 MGLSWSPRPPLMLILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYQH 60
QY 61 LGSCTSSLSRPLPLEESAMSDCLEAAEQRLNSSLIDCRCHRRMKHQATCLDIYVTVHPA 120
Db 61 LGSCTSSLSRPLPLEESAMSDCLEAAEQRLNSSLIDCRCHRRMKHQATCLDIYVTVHPA 120
QY 121 RSLGDYELDVSPYEDTVTSKPKWNLSKLNMLKPDSDLCLFKFAMLC TLHDKCDRLRKAYG 180
Db 121 RSLGDYELDVSPYEDTVTSKPKWNLSKLNMLKPDSDLCLFKFAMLC TLHDKCDRLRKAYG 180
QY 181 EACSGIRCORHICLAQLRSFFKAEASHAQGLLLCFCAPEDAGCGERRNTIAPSCALPS 240
-Db 181 EACSGIRCORHICLAQLRSFFKAEASHAQGLLLCFCAPEDAGCGERRNTIAPSCALPS 240
QY 241 VTPNCLDLSRCFADPLCRSLMDFTQCHPMDIILGTGTCATOSRCILRAYGLIGTAMTPN 300
Db 241 VTPNCLDLSRCFADPLCRSLMDFTQCHPMDIILGTGTCATOSRCILRAYGLIGTAMTPN 300
QY 301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKWRFHRLFSQDWADS 360
Db 301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKWRFHRLFSQDWADS 360
QY 361 TFSVVQOQNSNPALRLQPLRPILSFIPLILLQTLW 397
Db 361 TFSVVQOQNSNPALRLQPLRPILSFIPLILLQTLW 397

RESULT 2
AA084591
ID AA084591 standard; protein; 397 AA.
XX
XX AA084591;
DT 25-JUL-2000 (first entry)
XX
DE Amino acid sequence of a human growth factor receptor-alpha precursor.
XX
KW Human; artemin; growth factor; neurotrophic factor; trophic support;
KW neuron; trigeminal ganglion neuron; nodose ganglion neuron;
KW superior cervical ganglion neuron; midbrain neuron; Alzheimer's disease;
KW peripheral neuropathy; amyotrophic lateral sclerosis; ischemic stroke;
KW Parkinson's disease; Huntington's disease; acute brain injury;
KW acute spinal cord injury; nervous system tumour; blastoma;
KW multiple sclerosis; infection; enteric disease; idiopathic constipation;
KW Parkinson's disease; small cell lung carcinoma.
XX

Mus sp.
XX
XX Key Location/Qualifiers
FH Peptide 1..28 /note= "signal peptide"
FT Protein 29..369 /note= "mature protein"
FT Modified-site 92 /note= "putative N-linked glycosylation site"
FT Modified-site 145 /note= "putative N-linked glycosylation site"
FT Modified-site 306 /note= "putative N-linked glycosylation site"
WO200018799-A1.
XX
PD 06-APR-2000.
XX
PF 29-SEP-1999; 99WO-US022604.
XX
PR 29-SEP-1998; 98US-00163283.
PR 12-NOV-1998; 98US-0108148P.
PR 22-DEC-1998; 98US-00218698.
XX (UNIW) UNIV WASHINGTON.
XX
XX Milbrandt JD, Baloh RH;
XX WPI; 2000-293109/25.
XX
XX Isolated artemin growth factor proteins and the nucleic acids that encode
PT them, useful for treating a range of degenerative neuronal disorders such
PT as Parkinson's disease and Huntington's disease.
XX
XX Disclosure; Fig 12; 96pp; English.
XX
CC The present sequence represents a murine growth factor receptor-alpha
CC precursor. The specification describes an artemin growth factor protein.
CC Artemin is a neurotrophic factor that belongs to the GDNF (glial cell
CC line-derived neurotrophic factor)/neurturin/persephin family of growth
CC factors and promotes differentiation, maintains mature phenotype and
CC provides trophic support, promoting growth and survival of neurons.
CC Artemin promotes the survival of trigeminal ganglion neurons, nodose
CC ganglion neurons, superior cervical ganglion neurons and tyrosine-
CC hydroxylase-expressing dopaminergic ventral midbrain neurons. Artemin is
CC the only member of the GDNF family that binds to GFR-alpha (growth factor
CC receptor-alpha) and activates the GFR-alpha3/RET (Ret protein- tyrosine
CC kinase) receptor complex and additionally, like GDNF and neurturin,
CC artemin also binds to and activates GFRalpha/RET. Artemin polypeptides
CC and polynucleotides are administered to treat peripheral neuropathy,
CC amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease,
CC Huntington's disease, ischemic stroke, acute brain injury, acute spinal
CC cord injury, a nervous system tumour (e.g. blastoma), multiple
CC sclerosis, infection or enteric disease (e.g. idiopathic constipation or
CC constipation associated with Parkinson's disease, spinal cord injury or
CC use of opiate pain killers). They may also be used to treat a patient
CC suffering from small cell lung carcinoma
XX
XX Sequence 397 AA;

Query Match 100.0%; Score 2131; DB 3; Length 397;
Best Local Similarity 100.0%; Pred. No. 3.5e-198;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSWSPRPPLMLILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYQH 60
Db 1 MGLSWSPRPPLMLILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYQH 60
QY 61 LGSCTSSLSRPLPLEESAMSDCLEAAEQRLNSSLIDCRCHRRMKHQATCLDIYVTVHPA 120
Db 61 LGSCTSSLSRPLPLEESAMSDCLEAAEQRLNSSLIDCRCHRRMKHQATCLDIYVTVHPA 120
QY 121 RSLGDYELDVSPYEDTVTSKPKWNLSKLNMLKPDSDLCLFKFAMLC TLHDKCDRLRKAYG 180

Db 121 RSLGDELVSYPEDTTSKPKWNLKLNMLKPDSDLCFKFAMLCITLHDKCDRLRKAYG 180
Qy 181 EACSGICORHLCLAQLSFFPEKAESAHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240
Db 181 EACSGICORHLCLAQLSFFPEKAESAHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240
Qy 241 VTPNCLDLRSFCRADPLCRSLMDFTQCHPMDILGTCAEQSLRAYLGLIGTAMTPN 300
Db 241 VTPNCLDLRSFCRADPLCRSLMDFTQCHPMDILGTCAEQSLRAYLGLIGTAMTPN 300
Qy 301 FISKVNTTVALSCTCRSGNLQDECEQLERSFSONPCLVEIAAKMRPHRQLFSQDWADS 360
Db 301 FISKVNTTVALSCTCRSGNLQDECEQLERSFSONPCLVEIAAKMRPHRQLFSQDWADS 360
Qy 361 TFSVVQOQNSNPALRQLPILSILPLLQLTLW 397
Db 361 TFSVVQOQNSNPALRQLPILSILPLLQLTLW 397

RESULT 3
AA15174
ID AA15174 standard; protein; 397 AA.
AC AA15174;
XX
DT 07-FEB-2000 (first entry)
XX
DE Murine GFRalpha3.
XX
KW Murine GFRalpha3; GFRalpha3;
KW glial-cell-line-derived neurotrophic factor family receptor alpha-3;
KW probe; homologous DNA; neuronal cell activation; GFRalpha3 ligand;
KW cell proliferation; cell differentiation; GFRalpha3-containing cell;
KW Ret-containing cell; peripheral nervous system disease; diabetes;
KW human immunodeficiency virus; chemotherapeutic agent treatment;
KW autonomic nervous system dysfunction; transgenic animal.
XX
OS Mus musculus.
XX
XX
Key Location/Qualifiers
FT Peptide 1..27
FT /label= Signal_peptide
FT Modified-site 92..95
FT /note= "Potential glycosylation site"
FT Modified-site 145..148
FT /note= "Potential glycosylation site"
FT Region 392..397
FT /note= "C-terminal hydrophobic sequence associated with GPI-anchoring"
XX
XX WO9949039-A2.
XX
XX 30-SEP-1999.
XX
XX 19-MAR-1999; 99WO-US006098.
XX
XX 23-MAR-1998; 98US-0079124P.
XX 13-APR-1998; 98US-0081569P.
XX
XX (GETH) GENENTECH INC.
XX
XX De Sauvage FJ, Klein RD, Phillips HS, Rosenthal A;
XX WPI; 2000-038358/03.
XX N-ESDB; AAZ29100.
XX
XX New isolated GFR-alpha3 nucleic acid, used to develop products for
XX treating diseases or conditions involving peripheral nervous system or
XX autonomic nervous system.
XX
XX Example 1; Fig 1; 112pp; English.

CC The present sequence is the full length mouse glial-cell-line-derived
CC neurotrophic factor family receptor alpha-3 (GFRalpha3). This has
CC sequence identity with GFRalpha3 DNA or its fragments can be
CC used as a probe to screen for homologous DNA. GFRalpha3 possess neuronal
CC cell activation property. GFRalpha3 ligands can be used to stimulate
CC proliferation, growth, survival, differentiation, metabolism or
CC regeneration of GFRalpha3- and Ret-containing cells. They can be useful
CC in the treatment of peripheral nervous system diseases, eg. those
CC associated with diabetes, human immunodeficiency virus, or
CC chemotherapeutic agent treatments. Agonist or antagonists of GFRalpha3
CC can be used to treat autonomic nervous system dysfunctions. The products
CC can also be used for detection, diagnosis and production of transgenic
CC animals
XX
SQ Sequence 397 AA;
Query Match 100.0%; Score 2131; DB 3; Length 397;
Best Local Similarity 100.0%; Pred. No. 3.5e-198;
Matches 397; Conservative 0; -Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGLSWSRPPLLLMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYQH 60
Db 1 MGLSWSRPPLLLMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYQH 60
Qy 61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLENSSLIDCRCHRRMKHQATCLDIYTVHPA 120
Db 61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLENSSLIDCRCHRRMKHQATCLDIYTVHPA 120
Qy 121 RSLGDELVSYPEDTTSKPKWNLKLNMLKPDSDLCFKFAMLCITLHDKCDRLRKAYG 180
Db 121 RSLGDELVSYPEDTTSKPKWNLKLNMLKPDSDLCFKFAMLCITLHDKCDRLRKAYG 180
Qy 181 EACSGICORHLCLAQLSFFPEKAESAHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240
Db 181 EACSGICORHLCLAQLSFFPEKAESAHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240
Qy 241 VTPNCLDLRSFCRADPLCRSLMDFTQCHPMDILGTCAEQSLRAYLGLIGTAMTPN 300
Db 241 VTPNCLDLRSFCRADPLCRSLMDFTQCHPMDILGTCAEQSLRAYLGLIGTAMTPN 300
Qy 301 FISKVNTTVALSCTCRSGNLQDECEQLERSFSONPCLVEIAAKMRPHRQLFSQDWADS 360
Db 301 FISKVNTTVALSCTCRSGNLQDECEQLERSFSONPCLVEIAAKMRPHRQLFSQDWADS 360
Qy 361 TFSVVQOQNSNPALRQLPILSILPLLQLTLW 397
Db 361 TFSVVQOQNSNPALRQLPILSILPLLQLTLW 397
RESULT 4
ADJ58709
ID ADJ58709 standard; protein; 397 AA.
XX
AC ADJ58709;
XX
DT 06-MAY-2004 (first entry)
XX
DE Murine retL3 protein.
XX
KW Tissue growth; retL protein; organ failure; foetal malformation;
KW tumour growth; renal tissue; cytostatic; vulnery; nephrotropic; murine.
XX
XX Mus sp.
XX US6677135-B1.
XX
XX 13-JAN-2004.
XX
XX 06-NOV-1998; 98US-00187906.
XX
XX 08-MAY-1996; 96US-0017427P.
XX 07-JUN-1996; 96US-0019300P.
XX 16-JUL-1996; 96US-0021859P.

PR 23-AUG-1996; 96US-0023444P.
 PR 11-APR-1997; 97US-0043533P.
 PR 07-MAY-1997; 97WO-US0007726.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
 XX
 DR WPI; 2004-079845/08.
 DR N-PSDB; ADJ58708.
 XX
 PT New nucleic acid encoding Ret polypeptide, useful for diagnosing and/or
 PT treating diseases or conditions associated with aberrant expression or
 PT activity of the Ret ligand, such as organ failure, fetal malformations
 PT and tumor growth.
 XX
 PS Claim 1; SEQ ID NO 17; 66pp; English.
 XX
 CC The present invention relates to nucleotide and amino acid sequences
 CC which promote tissue growth and methods for modulating tissue growth. The
 CC invention also relates to retL proteins and polynucleotides encoding such
 CC proteins. RetL proteins interact with a receptor protein Ret to trigger
 CC dimerization and/or autophosphorylation of the tyrosine kinase domain of
 CC the receptor protein Ret. The methods and compositions of the present
 CC invention are useful for the diagnosis and/or treatment of diseases or
 CC conditions associated with aberrant expression or activity of the Ret
 CC ligand, such as organ failure, foetal malformations and tumour growth and
 CC for promoting regeneration or survival of damaged renal tissue. The
 CC present sequence is murine retL3 protein of the invention.
 XX
 SQ Sequence 397 AA;

Query Match 100.0%; Score 2131; DB 8; Length 397;
 Best Local Similarity 100.0%; Pred. No. 3.5e-198;
 Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGLSWSPRPPLMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYQH 60
 DB 1 MGLSWSPRPPLMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYQH 60
 QY 61 LGSCTSSLSRPLPLEESAMSDCLEAEOLRNSLIDCRCHRMKHOATCLDIYVTVHPA 120
 DB 61 LGSCTSSLSRPLPLEESAMSDCLEAEOLRNSLIDCRCHRMKHOATCLDIYVTVHPA 120
 QY 121 RSLGDIYELDVSPYEDVTVTSKPKWNLKLNMLKPDSDLCLEAEOLRNSLIDCRCHRMKHOATCLDIYVTVHPA 180
 DB 121 RSLGDIYELDVSPYEDVTVTSKPKWNLKLNMLKPDSDLCLEAEOLRNSLIDCRCHRMKHOATCLDIYVTVHPA 180
 QY 181 EACSGIRCQRHLCLAQLSRFFFEKAAESHAQGLLLCPEDAGCGERRNTIAPSCALPS 240
 DB 181 EACSGIRCQRHLCLAQLSRFFFEKAAESHAQGLLLCPEDAGCGERRNTIAPSCALPS 240
 QY 241 VTPNCLDLRSFCRADPLCRSLRMDFOCHPMDILGTGTCATEOSRCIRAYLGLIGTAMTN 300
 DB 241 VTPNCLDLRSFCRADPLCRSLRMDFOCHPMDILGTGTCATEOSRCIRAYLGLIGTAMTN 300
 QY 301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRPHRQLFSQDWADS 360
 DB 301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRPHRQLFSQDWADS 360
 QY 361 TFSVVOQQNSNPALRQLRPLPILSILPILLIQTILW 397
 DB 361 TFSVVOQQNSNPALRQLRPLPILSILPILLIQTILW 397

RESULT 5
 ADY53845
 ID ADY53845 standard; protein; 397 AA.
 XX
 AC ADY53845;
 XX
 DT 05-MAY-2005 (first entry)
 XX

DE Mouse retL3 protein.
 XX DNA purification; immune stimulation; ret ligand.
 XX
 OS Mus sp.
 XX
 PN US6861509-B1.
 XX
 PD 01-MAR-2005.
 XX
 PF 21-JAN-2000; 2000US-00489407.
 XX
 PR 08-MAY-1996; 96US-0017427P.
 PR 07-JUN-1996; 96US-0019300P.
 PR 16-JUL-1996; 96US-0021859P.
 PR 23-AUG-1996; 96US-0023444P.
 PR 11-APR-1997; 97US-0043533P.
 PR 07-MAY-1997; 97WO-US0007726.
 PR 06-NOV-1998; 98US-00187906.
 XX
 XX (BIOJ) BIOGEN INC.
 PA
 PI Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
 XX
 DR WPI; 2005-201184/21.
 DR N-PSDB; ADY53844.
 XX
 PT New anti-Ret ligand (RetL) antibody, useful for treating acute renal
 PT failure, acute nephritis, chronic renal failure, nephritic syndrome, as
 PT well as Alzheimer's disease, Parkinson's and multiple sclerosis.
 XX
 PS Disclosure; SEQ ID NO 17; 66pp; English.
 XX
 CC The invention relates to an antibody produced by a hybridoma selected
 CC from the group consisting of AA.P9 and AA.GE7.3. The antibody is used to
 CC stimulate neural and renal cell growth. This sequence corresponds to a
 CC protein sequence of the invention.
 XX
 SQ Sequence 397 AA;
 Query Match 100.0%; Score 2131; DB 9; Length 397;
 Best Local Similarity 100.0%; Pred. No. 3.5e-198;
 Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGLSWSPRPPLMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYQH 60
 DB 1 MGLSWSPRPPLMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYQH 60
 QY 61 LGSCTSSLSRPLPLEESAMSDCLEAEOLRNSLIDCRCHRMKHOATCLDIYVTVHPA 120
 DB 61 LGSCTSSLSRPLPLEESAMSDCLEAEOLRNSLIDCRCHRMKHOATCLDIYVTVHPA 120
 QY 121 RSLGDIYELDVSPYEDVTVTSKPKWNLKLNMLKPDSDLCLEAEOLRNSLIDCRCHRMKHOATCLDIYVTVHPA 180
 DB 121 RSLGDIYELDVSPYEDVTVTSKPKWNLKLNMLKPDSDLCLEAEOLRNSLIDCRCHRMKHOATCLDIYVTVHPA 180
 QY 181 EACSGIRCQRHLCLAQLSRFFFEKAAESHAQGLLLCPEDAGCGERRNTIAPSCALPS 240
 DB 181 EACSGIRCQRHLCLAQLSRFFFEKAAESHAQGLLLCPEDAGCGERRNTIAPSCALPS 240
 QY 241 VTPNCLDLRSFCRADPLCRSLRMDFOCHPMDILGTGTCATEOSRCIRAYLGLIGTAMTN 300
 DB 241 VTPNCLDLRSFCRADPLCRSLRMDFOCHPMDILGTGTCATEOSRCIRAYLGLIGTAMTN 300
 QY 301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRPHRQLFSQDWADS 360
 DB 301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRPHRQLFSQDWADS 360
 QY 361 TFSVVOQQNSNPALRQLRPLPILSILPILLIQTILW 397
 DB 361 TFSVVOQQNSNPALRQLRPLPILSILPILLIQTILW 397

RESULT 6

ADZ00209
ID ADZ00209 standard; protein; 397 AA.

XX AC ADZ00209;

XX DT 30-JUN-2005 (first entry)

XX DE Mouse Ret ligand 3 (RetL3), SEQ ID NO:17.

XX KW Cell growth; development; signal transduction; neuroprotection; neurodegenerative disease; renal disease; genitourinary disease; neuroprotective; nephrotropic; cancer; neoplasm; cytostatic; RetL3;
XX KW Ret tyrosine kinase receptor ligand 3; Ret ligand 3;
XX KW GDNF family receptor alpha 3; GFR3.

XX OS Mus sp.

XX PN US2005080235-A1.

XX PD 14-APR-2005.

XX PF 23-SEP-2003; 2003US-00668936.

XX PR 08-MAY-1996; 96US-0017427P.

XX PR 07-JUN-1996; 96US-0019300P.

XX PR 16-JUL-1996; 96US-0021859P.

XX PR 23-AUG-1996; 96US-0023444P.

XX PR 11-APR-1997; 97US-0043533P.

XX PR 07-MAY-1997; 97WO-US007726.

XX PR 06-NOV-1998; 98US-00187906.

XX PA (SANI//) SANICOLA-NADEL M.

XX PA (HESS//) HESSION C.

XX PA (CATE//) CATE R L.

XX PA (WORL//) WORLEY D S.

XX PI Sanicola-Nadel M, Hession C, Cate RL, Worley DS;

XX DR WPI; 2005-305025/31.

XX DR N-PSDB; ADZ00208.

XX FT New polypeptide sequence that interacts with a receptor protein Ret to

XX PT trigger dimerization or autophosphorylation, useful in preparing a

XX PT composition for treating neurodegenerative disorders, e.g., Alzheimer's

XX PS disease.

XX PS Claim 1; SEQ ID NO 17; 67pp; English.

XX PS The invention relates to the murine and human RetL3 (Ret ligand 3)

XX CC proteins (ADZ00209 and ADZ00213, respectively) and to proteins at least

XX CC 80% identical to murine or human RetL3. The invention also discloses

XX CC other RetL3 proteins such as rat RetL1, human RetL1, human RetL2,

XX CC fragments of human RetL1, mouse RetL3 and human RetL3, and cDNA sequences

XX CC encoding these RetL3 proteins or protein fragments. Like other RetL

XX CC proteins, the RetL3 proteins of the invention interact with the Ret

XX CC receptor tyrosine kinase that is encoded by the Ret proto-oncogene.

XX CC triggering Ret receptor dimerization or autophosphorylation. The Ret

XX CC receptor is expressed during development in a variety of tissues,

CC

-expressing tumors. Anti-RetL antibodies and RetL fusion proteins may also be used in medical imaging. The present sequence represents a specifically claimed full-length murine RetL3 protein encoded by cDNA isolated in the invention.

XX SQ Sequence 397 AA;

Query Match 100.0%; Score 2131; DB 9; Length 397;

Best Local Similarity 100.0%; Pred. No. 3.5e-198;

Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSWSPRPPLLMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYOH 60

DB 1 MGLSWSPRPPLLMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYOH 60

QY 61 LGSCTSSLSRPLPLEESAMSDCLEAAEOLRNSSLIIDCRCHRRMKHQATCLDIYVTHPA 120

DB 61 LGSCTSSLSRPLPLEESAMSDCLEAAEOLRNSSLIIDCRCHRRMKHQATCLDIYVTHPA 120

QY 121 RSLGDYELDVSPYEDTIVTSKPKWNLSKLNMLKPDSDILCLKFAMLCTLHDKCDRLRKAYG 180

DB 121 RSLGDYELDVSPYEDTIVTSKPKWNLSKLNMLKPDSDILCLKFAMLCTLHDKCDRLRKAYG 180

QY 181 EACSGIRCORHLCLAQLRSPFEKAEASHAQGLLLCPAPEDAGCERRRNTIAPSCALPS 240

DB 181 EACSGIRCORHLCLAQLRSPFEKAEASHAQGLLLCPAPEDAGCERRRNTIAPSCALPS 240

QY 241 VTPNCLDLRSPCRADPLCRSLRMDPQTHCHPMDILGTCAEQSLRAYLGLIGTAMTPN 300

DB 241 VTPNCLDLRSPCRADPLCRSLRMDPQTHCHPMDILGTCAEQSLRAYLGLIGTAMTPN 300

QY 301 FISKVNTTVALSCTCRSGNLQDECEQLERSFSQNPCLVEIAAAMRFRHQLFSQDWADS 360

DB 301 FISKVNTTVALSCTCRSGNLQDECEQLERSFSQNPCLVEIAAAMRFRHQLFSQDWADS 360

QY 361 TFSVVOQONSNPALRQLPRLPILSILPLILLQLTLW 397

DB 361 TFSVVOQONSNPALRQLPRLPILSILPLILLQLTLW 397

RESULT 7

AAW84182

ID AAW84182 standard; protein; 397 AA.

XX AC AAW84182;

XX DT 25-MAR-1999 (first entry)

XX DE A GDNFR-alpha-related protein 3 (GRR3).

XX KW Rat; glial cell-line derived neurotrophic factor receptor; GDNFR;

XX KW glial cell line-derived neurotrophic factor; GDNF; neurturin;

XX KW signal transduction; dopaminergic nerve cell; Parkinson's disease;

XX KW Alzheimer's disease; amyotrophic lateral sclerosis;

XX KW neurological disorder; diabetes; glaucoma; sensory neuron;

XX KW retinal ganglion cell degeneration; sensory neuropathy; retinopathy;

XX KW gene therapy; GDNFR-related protein 3; GRR3.

XX OS Rattus sp.

XX PN WO9854213-A2.

XX PD 03-DEC-1998.

XX PF 27-APR-1998; 98WO-US008486.

XX PR 30-MAY-1997; 97US-00866354.

XX PA (AMGE-) AMGEN INC.

XX PI Fox GM, Jing S, Wen D;

XX DR WPI; 1999-080806/07.

DR N-PSDB; AAV99331.
 XX New isolated glial cell line-derived neurotrophic factor receptors - used
 PT to develop products for treating e.g. improperly functioning dopaminergic
 PT nerve cells, Parkinson's disease, Alzheimer's disease or amyotrophic
 PT lateral sclerosis.
 XX
 XX Claim 51; Fig 17; 318pp; English.
 PS
 XX The present sequence represents a rat glial cell-line derived
 CC neurotrophic factor receptor (GDNFR)-related protein 3 (GRR3). The
 CC protein has similar functions to GDNFR. GDNFR proteins are functionally
 CC characterised by the ability to bind glial cell line-derived neurotrophic
 CC factor (GDNF) and/or neuritin specifically, and to act as part of a
 CC molecular complex which mediates or enhances the signal transduction
 CC affects of GDNF and/or neuritin. The proteins can be used for treating
 CC Alzheimer's disease or amyotrophic lateral sclerosis. They can also be
 CC used for treating neurological disorders associated with diabetes,
 CC glaucoma or other diseases and conditions involving retinal ganglion cell
 CC degeneration, sensory neuropathy caused by injury to, insults to, or
 CC degeneration of, sensory neurons, pathological conditions, or disease or
 CC injury-related retinopathies. The products can also be used for
 CC detection, diagnosis, drug screening and gene therapy
 XX
 XX Sequence 397 AA;

Query Match 92.5%; Score 1972; DB 2; Length 397;
 Best Local Similarity 92.9%; Pred. No. 1e-182;
 Matches 369; Conservative 9; Mismatches 19; Indels 0; Gaps 0;
 QY 1 MGLSWSPRLMILLVLSLPLGAGNSLATENRFVNSCTQARKKCEANPACAAAYOH 60
 DB 1 MGLSRSPRPPLVILLVLSLPLGAGNSLATENRFVNSCTQARKKCEANPACAAAYOH 60
 QY 61 LGSCTSSLSRPLPLEBSAMSDCLAEAEOLRNSLIDCRCHRMKHOATCLDIYWTVHPA 120
 DB 61 LGSCTPSLSPLPSGESATSAACLEAQQRLNSSLIDCRCHRMKHOATCLDIYWTVHPV 120
 QY 121 RSLGDIYELVSPYEDVTTSKPMNLSKLNMLKPSDCLCLKFAMLTCLHDKCDRLRKAYG 180
 DB 121 RSLGDIYELVSPYEDVTTSKPMNLSKLNMLKPSDCLCLKFAMLTCLHDKCDRLRKAYG 180
 QY 181 EACSGIRCORHCLQAQLRSFFFEKAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240
 DB 181 EACSGIRCORHCLQAQLRSFFFEKAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240
 QY 241 VTPNCLDLRSFCRADPLCRSLMDFOTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTN 300
 DB 241 VAPNCLDLRSFCRADPLCRSLMDFOTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTN 300
 QY 301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHQLFSQDWDAS 360
 DB 301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHQLFSQDWDAS 360
 QY 361 TFSVVOQQNSPALRLOPLPILSPILPILLOTLW 397
 DB 361 TFSVVOQQNSPALRLOPLPILSPILPILLOTLW 397

RESULT 8
 AAY15182
 ID AAY15182 standard; protein; 888 AA.
 AC AAY15182;
 XX
 XX 07-FEB-2000 (first entry)
 DT
 XX gD-GFRalpha3-Rse-gD chimeric receptor.
 DE
 XX gD-GFRalpha3-Rse-gD chimeric receptor; gD epitope tag; murine GFRalpha3;
 KW GPI signal; human GFRalpha3; Rse tyrosine kinase receptor; psvi vector;
 KW recombinant PCR; SV40 promoter; agonist antibody; natural ligand.

XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH 110.386
 FT Region /note="Ligand binding region"
 FT
 XX WO9949039-A2.
 PN
 XX 30-SEP-1999.
 PD
 XX 19-MAR-1999; 99WO-US006098.
 PF
 XX 23-MAR-1999; 98US-0079124P.
 PR
 XX 13-APR-1999; 98US-0081569P.
 XX (GETH) GENENTECH INC.
 PA
 XX De Sauvage FJ, Klein RD, Phillips HS, Rosenthal A;
 PI WPI; 2000-038358/03.
 DR
 XX New isolated GFR-alpha3 nucleic acid, used to develop products for
 PT treating diseases or conditions involving peripheral nervous system or
 PT automic nervous system.
 PT
 XX Claim 9; Page 107-110; 112pp; English.
 PS
 XX The present sequence is gD-GFRalpha3-Rse-gD chimeric receptor. This was
 CC constructed with the gD epitope tag followed by the murine GFRalpha3
 CC extracellular domain (less the GPI signal; preferably the human
 CC GFRalpha3) followed by the transmembrane and intracellular domain of the
 CC Rse tyrosine kinase receptor and another gD epitope tag. This construct
 CC was assembled by recombinant PCR into a psvi vector under the control of
 CC the SV40 promoter. This is used in an assay to identify agonist
 CC antibodies and a natural ligand for mammalian GFRalpha3
 XX
 XX Sequence 888 AA;

Query Match 88.2%; Score 1880; DB 3; Length 888;
 Best Local Similarity 94.1%; Pred. No. 2.8e-173;
 Matches 354; Conservative 5; Mismatches 11; Indels 6; Gaps 1;
 QY 25 LGAGNSLATENRFVNSCTQARKKCEANPACAAAYOHLSCTSSLSRPLPLEBSAMSDCL 84
 DB 54 LEAGNSLATENRFVNSCTQARKKCEANPACAAAYOHLSCTSSLSRPLPLEBSAMSDCL 113
 QY 85 EAAEOLRNSLIDCRCHRMKHOATCLDIYWTVHPARSLGDIYELVSPYEDVTTSKPMK 144
 DB 114 EAAEOLRNSLIDCRCHRMKHOATCLDIYWTVHPARSLGDIYELVSPYEDVTTSKPMK 173
 QY 145 NLSKLNMLKPSDCLCLKFAMLTCLHDKCDRLRKAYGEACSGIRCORHCLQAQLRSFFFEKA 204
 DB 174 NLSKLNMLKPSDCLCLKFAMLTCLHDKCDRLRKAYGEACSGIRCORHCLQAQLRSFFFEKA 233
 QY 205 AESHAQGLLLCPAPEDAGCGERRNTIAPSCALPSVTPNCLDLRSFCRADPLCRSLMD 264
 DB 234 AESHAQGLLLCPAPEDAGCGERRNTIAPSCALPSVTPNCLDLRSFCRADPLCRSLMD 293
 QY 265 FOTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTNFISKVNTTVALSCTCRGSGNLQDE 324
 DB 294 FOTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTNFISKVNTTVALSCTCRGSGNLQDE 353
 QY 325 CEQLERSFSQNPCLVEAIAAKMRFHQLFSQDWDASTFSVVOQQNSPALR-----LOP 378
 DB 354 CEQLERSFSQNPCLVEAIAAKMRFHQLFSQDWDASTFSVVOQQNSPALRPAWVPVLGV 413
 QY 379 RLPILSPILPILLO 394
 DB 414 LTALVTAALAILLR 429
 RESULT 9

AAW37465
 ID AAW37465 standard; protein; 346 AA.
 AC AAW37465;
 XX
 XX 21-MAY-1998 (first entry)
 XX
 XX Mouse Ret ligand retL3 partial sequence.
 XX
 XX Ret ligand; RetL3; receptor; signal transduction; mouse;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury; neurodegeneration;
 KW motor neuron disease; multiple sclerosis; infection; meningitis;
 KW myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury;
 KW spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease;
 KW muscular dystrophy; myasthenia gravis; tumour; therapy.
 XX
 XX Mus musculus.
 XX
 XX WO9744356-A2.
 XX
 XX 27-NOV-1997.
 XX
 XX 07-MAY-1997; 97WO-US007726.
 XX
 XX 08-MAY-1996; 96US-0017427P.
 PR 07-JUN-1996; 96US-0019300P.
 PR 16-JUL-1996; 96US-0021859P.
 PR 11-APR-1997; 97US-0043533P.
 XX
 XX (BIOJ) BIOGEN INC.
 XX
 XX Sanicola-Nadel M, Hession C, Cate RL;
 XX WPI; 1998-018431/02.
 DR N-PSDB; AAW00256.
 XX
 XX New nucleic acid encoding ret receptor ligands and related proteins -
 PT vectors, transformed cells and antibodies, used for promoting cell growth
 PT and improving survival of injured cells, especially renal or nerve cells.
 XX
 XX Disclosure; Page 73-74; 113pp; English.
 XX
 XX This polypeptide comprises a partial sequence of mouse Ret ligand RetL3,
 CC deduced from EST AA050083 cDNA (see AAW00256). A full-length mouse RetL3
 CC sequence (see AAW37461) was also obtained. Rat, mouse and human retL1,
 CC retL2 and retL3 cDNA sequences (see AA00245-51) and encoded polypeptides
 CC (see AAW37457-63) are claimed and can be used in methods for promoting
 CC cell growth and improving survival of cells, especially renal or neural
 CC cells
 XX
 XX Sequence 346 AA;
 SQ
 Query Match 83.2%; Score 1774; DB 2; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1.6e-163;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 68 LSRPLPLEESAMSADCLEAAEQRLNSLIDCRCHRRMKHQATCLDIYTWVHPARSLGDYE 127
 DB 17 LSRPLPLEESAMSADCLEAAEQRLNSLIDCRCHRRMKHQATCLDIYTWVHPARSLGDYE 76
 QY 128 LDVSPYEDTTSKPKWKNLSKLNMLKPDSDCLKFAMLCITLHDKCDRLKAYGEACSGIR 187
 DB 77 LDVSPYEDTTSKPKWKNLSKLNMLKPDSDCLKFAMLCITLHDKCDRLKAYGEACSGIR 136
 QY 188 CORHCLQAQLRSFPEKAESAHAQGLLCPAPEDAGCGERRNTIAPSCALPSVTPNCLD 247
 DB 137 CORHCLQAQLRSFPEKAESAHAQGLLCPAPEDAGCGERRNTIAPSCALPSVTPNCLD 196
 QY 248 LRSFCRADPLCRSLMDFOTHCHPMDILGTCTATEQSCLRAYLGLIGTANTPFISKVNT 307
 DB 197 LRSFCRADPLCRSLMDFOTHCHPMDILGTCTATEQSCLRAYLGLIGTANTPFISKVNT 256

308 TVALSCTCRGSGNLQDECEQLERSFSQNPCLVIAAAMRHRQLFSQDWADSTFSVVQQ 367
 DB 257 TVALSCTCRGSGNLQDECEQLERSFSQNPCLVIAAAMRHRQLFSQDWADSTFSVVQQ 316
 QY 368 QNSNPALRQLPRLPILSILPLILLQTLW 397
 DB 317 QNSNPALRQLPRLPILSILPLILLQTLW 346

RESULT 10
 ADJ58707
 ID ADJ58707 standard; protein; 346 AA.
 XX
 XX ADJ58707;
 XX
 XX 06-MAY-2004 (first entry)
 XX
 XX Murine retL3 partial protein.
 DE
 XX
 KW Tissue growth; retL protein; organ failure; foetal malformation;
 KW tumour growth; renal tissue; cytostatic; vulnary; nephrotropic; murine.
 XX
 XX Mus sp.
 OS
 XX US6677135-B1.
 XX
 XX 13-JAN-2004.
 PD
 XX
 XX 06-NOV-1998; 98US-00187906.
 PF
 XX
 XX 08-MAY-1996; 96US-0017427P.
 PR 07-JUN-1996; 96US-0019300P.
 PR 16-JUL-1996; 96US-0021859P.
 PR 23-AUG-1996; 96US-0023444P.
 PR 11-APR-1997; 97US-0043533P.
 PR 07-MAY-1997; 97WO-US007726.
 XX
 XX (BIOJ) BIOGEN INC.
 PA
 XX
 XX Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
 PI
 XX WPI; 2004-079845/08.
 DR N-PSDB; ADJ58706.
 DR
 XX
 XX New nucleic acid encoding Ret polypeptide, useful for diagnosing and/or
 PT treating diseases or conditions associated with aberrant expression or
 PT activity of the Ret ligand, such as organ failure, fetal malformations
 PT and tumor growth.
 XX
 XX Disclosure; SEQ ID NO 15; 66pp; English.
 PS
 XX
 CC The present invention relates to nucleotide and amino acid sequences
 CC which promote tissue growth and methods for modulating tissue growth. The
 CC invention also relates to retL proteins and polynucleotides encoding such
 CC proteins. RetL proteins interact with a receptor protein Ret to trigger
 CC dimerisation and/or autophosphorylation of the tyrosine kinase domain of
 CC the receptor protein Ret. The methods and compositions of the present
 CC invention are useful for the diagnosis and/or treatment of diseases or
 CC conditions associated with aberrant expression or activity of the Ret
 CC ligand, such as organ failure, foetal malformations and tumour growth and
 CC for promoting regeneration or survival of damaged renal tissue. The
 CC present sequence is murine retL3 partial protein of the invention.
 XX
 XX Sequence 346 AA;
 SQ
 Query Match 83.2%; Score 1774; DB 8; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1.6e-163;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 68 LSRPLPLEESAMSADCLEAAEQRLNSLIDCRCHRRMKHQATCLDIYTWVHPARSLGDYE 127
 DB 17 LSRPLPLEESAMSADCLEAAEQRLNSLIDCRCHRRMKHQATCLDIYTWVHPARSLGDYE 76

QY 128 LDVSPYEDTVTSKPKWKNLSKLNMLKPDSDLCLEFAMLCITLHDKCDRLKAYGEACSGIR 187
 DB 77 LDVSPYEDTVTSKPKWKNLSKLNMLKPDSDLCLEFAMLCITLHDKCDRLKAYGEACSGIR 136
 QY 188 CORHCLLAQLRSFFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNCLD 247
 DB 137 CORHCLLAQLRSFFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNCLD 196
 QY 248 LRSFCRADPLCRSLRMDPQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFISKVNT 307
 DB 197 LRSFCRADPLCRSLRMDPQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFISKVNT 256
 QY 308 TVALSCTCRSGNLQDECEQLERSFSQNPCLVEIAAKMRFHRLQFSQDWADSTFSVVQQ 367
 DB 257 TVALSCTCRSGNLQDECEQLERSFSQNPCLVEIAAKMRFHRLQFSQDWADSTFSVVQQ 316
 QY 368 QNSNPALRLQPRLPILSILPLILLQTLW 397
 DB 317 QNSNPALRLQPRLPILSILPLILLQTLW 346

RESULT 11
 ADY53843
 ID ADY53843 standard; protein; 346 AA.

AC ADY53843;
 XX
 DT 05-MAY-2005 (first entry)
 DE Partial mouse retL3 protein.
 XX
 KW DNA purification; immune stimulation; ret ligand.
 XX
 OS Mus sp.

XX
 PN US6861509-B1.
 XX
 PD 01-MAR-2005.
 XX
 PF 21-JAN-2000; 2000US-00489407.

XX 08-MAY-1996; 96US-0017427P.
 PR 07-JUN-1996; 96US-0019300P.
 PR 16-JUL-1996; 96US-0021859P.
 PR 23-AUG-1996; 96US-0023444P.
 PR 11-APR-1997; 97US-0043533P.
 PR 07-MAY-1997; 97WO-US007726.
 PR 06-NOV-1998; 98US-00187906.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
 XX
 DR WPI; 2005-201184/21.
 DR N-PSDB; ADY53842.
 XX
 PT New anti-Ret ligand (RetL) antibody, useful for treating acute renal
 PT failure, acute nephritis, chronic renal failure, nephritic syndrome, as
 PT well as Alzheimer's disease, Parkinson's and multiple sclerosis.
 XX
 PS Disclosure; SEQ ID NO 15; 66pp; English.

XX
 CC The invention relates to an antibody produced by a hybridoma selected
 CC from the group consisting of AA.PF9 and AA.GE7.3. The antibody is used to
 CC stimulate neural and renal cell growth. This sequence corresponds to a
 CC protein sequence of the invention.

XX Sequence 346 AA;

Query Match 83.2%; Score 1774; DB 9; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1.6e-163;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 LSRPLPLEESAMSDCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDYE 127
 DB 17 LSRPLPLEESAMSDCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDYE 76
 QY 128 LDVSPYEDTVTSKPKWKNLSKLNMLKPDSDLCLEFAMLCITLHDKCDRLKAYGEACSGIR 187
 DB 77 LDVSPYEDTVTSKPKWKNLSKLNMLKPDSDLCLEFAMLCITLHDKCDRLKAYGEACSGIR 136
 QY 188 CORHCLLAQLRSFFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNCLD 247
 DB 137 CORHCLLAQLRSFFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNCLD 196
 QY 248 LRSFCRADPLCRSLRMDPQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFISKVNT 307
 DB 197 LRSFCRADPLCRSLRMDPQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFISKVNT 256
 QY 308 TVALSCTCRSGNLQDECEQLERSFSQNPCLVEIAAKMRFHRLQFSQDWADSTFSVVQQ 367
 DB 257 TVALSCTCRSGNLQDECEQLERSFSQNPCLVEIAAKMRFHRLQFSQDWADSTFSVVQQ 316
 QY 368 QNSNPALRLQPRLPILSILPLILLQTLW 397
 DB 317 QNSNPALRLQPRLPILSILPLILLQTLW 346

RESULT 12
 ADZ00207
 ID ADZ00207 standard; protein; 346 AA.

AC ADZ00207;
 XX
 DT 30-JUN-2005 (first entry)
 DE Mouse Ret ligand 3 (RetL3) fragment, SEQ ID NO:15.
 XX
 KW Cell growth; development; signal transduction; neurological disease;
 KW renal disease; genitourinary disease; neuroprotective; nephrotropic;
 KW cancer; neoplasm; cytosolic; RetL3;
 KW Ret tyrosine kinase receptor ligand 3; Ret ligand 3;
 KW GDNF family receptor alpha 3; GFRA3.

XX Mus sp.
 XX
 PN US2005080235-A1.
 XX
 PD 14-APR-2005.

PF 23-SEP-2003; 2003US-00668936.
 XX
 PR 08-MAY-1996; 96US-0017427P.
 PR 07-JUN-1996; 96US-0019300P.
 PR 16-JUL-1996; 96US-0021859P.
 PR 23-AUG-1996; 96US-0023444P.
 PR 11-APR-1997; 97US-0043533P.
 PR 07-MAY-1997; 97WO-US007726.
 PR 06-NOV-1998; 98US-00187906.

XX (SANI/) SANICOLA-NADEL M.
 PA (HESS/) HESSION C.
 PA (CATE/) CATE R L.
 PA (WORL/) WORLEY D S.

XX
 PI Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
 XX
 DR WPI; 2005-305025/31.
 DR N-PSDB; ADZ00206.

XX
 PT New polypeptide sequence that interacts with a receptor protein Ret to
 PT trigger dimerization or autophosphorylation, useful in preparing a
 PT composition for treating neurodegenerative disorders, e.g., Alzheimer's
 XX disease.
 PS Disclosure; SEQ ID NO 15; 67pp; English.

XX The invention relates to the murine and human RetL3 (Ret ligand 3)
 CC proteins (ADZ00209 and ADZ00213, respectively) and to proteins at least
 CC 80% identical to murine or human RetL3. The invention also discloses
 CC other RetL proteins such as rat RetL1, human RetL1, human RetL2,
 CC fragments of human RetL1, mouse RetL3 and human RetL3, and cDNA sequences
 CC encoding these RetL proteins or protein fragments. Like other RetL
 CC proteins, the RetL3 proteins of the invention interact with the Ret
 CC receptor tyrosine kinase that is encoded by the Ret proto-oncogene,
 CC triggering Ret receptor dimerization or autophosphorylation. The Ret
 CC receptor is expressed during development in a variety of tissues,
 CC including the peripheral and central nervous systems and the kidney. It
 CC is also expressed in some cancers. RetL proteins such as the murine and
 CC human RetL3 proteins, and RetL polynucleotides may be used for
 CC stimulating Ret receptor signaling, thereby promoting renal or neuronal
 CC cell growth or survival and minimizing damage to such tissues after
 CC various insults. They may therefore be used to treat renal disorders
 CC (e.g., renal failure, renal tube defects and renal trauma) or
 CC neurological disorders including neurodegenerative disorders (e.g.,
 CC Alzheimer's disease), bacterial or viral diseases of the nervous system
 CC (e.g., meningitis), neurological damage (e.g., that caused by hemorrhage
 CC or trauma) and developmental neural disorders (e.g., mental retardation).
 CC Conversely, antibodies against RetL may be used to block RetL-Ret
 CC receptor signal transduction for inhibiting tumor growth, fusion proteins
 CC comprising a RetL protein are useful for targeting a drug to Ret receptor
 CC -expressing tumors. Anti-RetL antibodies and RetL fusion proteins may
 CC also be used in medical imaging. The present sequence represents a murine
 CC RetL3 fragment encoded by a murine RetL3 partial cDNA initially
 CC identified by a search of an expressed sequence tag (EST) database using
 CC a rat RetL1 peptide sequence, and isolated from the EST clones AA049894
 CC and AA050083.
 XX Sequence 346 AA;

Query Match 83.2%; Score 1774; DB 9; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1.6e-163;

Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 68 LSRPLPLEESAMSDCLEAAEQLRNSSLIDCRCHRMKHQATCLDIYVTHPARSLGDYE 127
 Db 17 LSRPLPLEESAMSDCLEAAEQLRNSSLIDCRCHRMKHQATCLDIYVTHPARSLGDYE 76
 QY 128 LDVSPYEDTVTSKPKWMNLSKLNMLKPDSDLCCLKFAMLCITLHDKCDRLRKAYGEACSGIR 187
 Db 77 LDVSPYEDTVTSKPKWMNLSKLNMLKPDSDLCCLKFAMLCITLHDKCDRLRKAYGEACSGIR 136
 QY 188 CORHLCIAQLRSFFFEKAESHAQGLLCPAPEDAGCGERRRNTIAPSCALPSVTPNCLD 247
 Db 137 CORHLCIAQLRSFFFEKAESHAQGLLCPAPEDAGCGERRRNTIAPSCALPSVTPNCLD 196
 QY 248 LRSFCRADPLCRSLRMDFTQTHCPMDILGTCAEQSRCLRAYLGLIGTAMTPNFISKVNT 307
 Db 197 LRSFCRADPLCRSLRMDFTQTHCPMDILGTCAEQSRCLRAYLGLIGTAMTPNFISKVNT 256
 QY 308 TVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRPHRQLFSQDWDADSTFVVQQ 367
 Db 257 TVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRPHRQLFSQDWDADSTFVVQQ 316
 QY 368 QNSNPALRLQRLPILSPILPLILLQTLW 397
 Db 317 QNSNPALRLQRLPILSPILPLILLQTLW 346

RESULT 13

AAW65116
 ID AAW65116 standard; protein; 400 AA.

XX
 AC AAW65116;

DT 28-SEP-1998 (first entry)

XX Human GDNF alpha-3 receptor protein #1.

XX

KW Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;
 KW treatment; neurodegenerative disease; Parkinson's Disease; ALS; SMA;
 KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;
 KW Huntington's Disease; Alzheimer's Disease; diabetic neuropathy; muscle;
 XX muscular dystrophy; diagnostic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..400
 FT /label= GDNF alpha-3
 FT /note= "Partial sequence"
 XX
 PN EP846764-A2.
 XX
 PD 10-JUN-1998.
 XX
 PF 20-NOV-1997; 97EP-00309375.
 XX
 PR 27-NOV-1996; 96GB-00024677.
 PR 09-MAY-1997; 97GB-00009463.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Lawrence GMP;
 XX
 XX WPI; 1998-299980/27.
 XX N-PSDB; AAV35364.
 XX
 PT New factor alpha 3 receptor polypeptide and e.g. DNA and agonists - used
 PT to treat neuro degenerative diseases, muscular diseases and nerve and
 PT muscle trauma and in diagnostic assays.
 XX
 PS Claim 4; Fig 2; 22pp; English.
 XX
 CC This sequence represents a novel glial cell line-derived neurotrophic
 CC factor alpha-3 receptor (GDNF alpha-3). This protein can be used to treat
 CC e.g. neurodegenerative diseases (such as Parkinson's Disease, amyotrophic
 CC lateral sclerosis (ALS), spinal muscular atrophy (SMA), Huntington's
 CC Disease, Alzheimer's Disease, diabetic neuropathy), muscular diseases
 CC (including the muscular dystrophies) and nerve and muscle trauma and in
 CC diagnostic assays for such conditions
 XX
 SQ Sequence 400 AA;

Query Match 77.3%; Score 1646.5; DB 2; Length 400;
 Best Local Similarity 77.8%; Pred. No. 4.9e-151;

Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

QY 7 PRPP-LLMILLVLSLMLPLCAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSGCT 65
 Db 9 PLPPVLMILLVLSLMLPLCAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSGCT 68
 QY 66 SSLSRPLPLEESAMSDCLEAAEQLRNSSLIDCRCHRMKHQATCLDIYVTHPARSLGD 125
 Db 69 SSISTPLPSEEPSVPADCLEAAQQLRNSLIGCMCHRMKNQVACLDIYVTHPARSLGN 128
 QY 126 YELDVSPYEDTVTSKPKWMNLSKLNMLKPDSDLCCLKFAMLCITLHDKCDRLRKAYGEACSG 185
 Db 129 YELDVSPYEDTVTSKPKWMNLSKLNMLKPDSDLCCLKFAMLCITLHDKCDRLRKAYGEACSG 188
 QY 186 IRCORHLCIAQLRSFFFEKAESHAQGLLCPAPEDAGCGERRRNTIAPSCALPSVTPNC 245
 Db 189 PHCORHVCILRQLLTFFKAABEPHAQGLLCPAPEDAGCGERRRNTIAPSCALPSVTPNC 248
 QY 246 LDLRSFCRADPLCRSLRMDFTQTHCPMDILGTCAEQSRCLRAYLGLIGTAMTPNFISKV 305
 Db 249 LELRRLCFSDPLCRSLRMDFTQTHCPMDILGTCAEQSRCLRAYLGLIGTAMTPNFISNV 308
 QY 306 NTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRPHRQLFSQDWDADSTFVV 365
 Db 309 NTSVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRPHRQLFSQDWDADSTFVV 368

QY 366 QOQNSNPALRQPLRPILSFSILPILLOTW 397
 Db 369 AHQENPAVRPQWPVPSLFSCTLPILLLSLW 400
 RESULT 14
 AAW37463
 ID AAW37463 standard; protein; 400 AA.
 XX AAW37463;
 AC AAW37463;
 DT 21-MAY-1998 (first entry)
 DE Human Ret ligand RetL3.
 DE Human Ret ligand RetL3.
 KW Ret ligand; RetL3; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury; neurodegeneration;
 KW motor neurone disease; multiple sclerosis; infection; meningitis;
 KW myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury;
 KW spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease;
 KW muscular dystrophy; myasthenia gravis; tumour; therapy.
 XX Homo sapiens.
 XX OS
 XX PN WO9744356-A2.
 XX PD 27-NOV-1997.
 XX PF 07-MAY-1997; 97WO-US007726.
 XX PR 08-MAY-1996; 96US-0017427P.
 XX PR 07-JUN-1996; 96US-0019300P.
 XX PR 16-JUL-1996; 96US-0021859P.
 XX PR 11-APR-1997; 97US-0043533P.
 XX PA (BIOJ) BIOGEN INC.
 XX PI Sanicola-Nadel M, Hession C, Cate RL;
 XX WPI; 1998-018431/02.
 XX DR N-PSDB; AAV00251.
 XX PT New nucleic acid encoding ret receptor ligands and related proteins -
 PT vectors, transformed cells and antibodies, used for promoting cell growth
 PT and improving survival of injured cells, especially renal or nerve cells.
 XX Claim 2; Page 85-86; 113pp; English.
 XX This amino acid sequence comprises human Ret ligand (RetL) RetL3, deduced
 CC from cDNA clones (see AAV00251) isolated from a adult heart and spinal
 CC cord libraries. Rat and human RetL1, human RetL2 and mouse RetL3
 CC sequences (see AAW37457-62) are also claimed. Human RetL3 is 34.3%
 CC identical to human RetL1, 34.9% identical to human RetL2 and 76.8%
 CC identical to murine RetL3. Ret ligand is a key component of the Ret
 CC signalling pathway that specifically interacts with Ret receptor protein,
 CC triggering Ret dimerisation and/or autophosphorylation of the Ret
 CC tyrosine kinase domain. Vectors containing RetL3 DNA and prokaryotic or
 CC eukaryotic host cells transformed or transfected with these vectors are
 CC claimed, as well as a method for production of RetL3, its soluble
 CC variants and fusion proteins with a toxin, imageable compound or
 CC radionuclide. RetL3, optionally when expressed from vectors in vivo, is
 CC used to promote growth of new tissue and survival of damaged tissue,
 CC particularly kidney or neural tissue. Typical applications are in renal
 CC failure, nephritis, kidney transplants, toxic or hypoxic injury,
 CC neurodegeneration, motor neurone disease, multiple sclerosis, bacterial,
 CC viral or prion infections (e.g. meningitis, myelopathy associated with
 CC HIV or Creutzfeldt-Jakob disease), cranial nerve or spinal cord injury,
 CC developmental disorders such as Down's syndrome and cerebral palsy, or
 CC conditions involving the peripheral nervous system (Lyme disease,
 CC muscular dystrophy and myasthenia gravis). Fusion proteins are used to
 CC deliver toxins etc. to Ret-expressing cells, especially tumours

SQ Sequence 400 AA;
 Query Match 77.3%; Score 1646.5; DB 2; Length 400;
 Best Local Similarity 77.8%; Pred. No. 4.9e-151;
 Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;
 QY 7 PRPP-LLMILLVLSLWPLGAGNSLATENFVNSCTOARKKCEANPACKAAYOHLGSGT 65
 Db 9 PLPPVVLMLLLPLPSPPLAAGDPLPTESRLMNSCLQARRKQADPTCSAAYHLLDSC 68
 QY 66 SSLSRPLPESAMADCLEAAEQLRNSSLIDCRCHRMKHQATCLDIYTVVHPARSLGD 125
 Db 69 SSISTPLPSEPSVPADCLEAAQQLRNSLLIGCMCHRRMKQVACLDIYTVVHRRASLGN 128
 QY 126 YELDVSPYEDVTGSKPWKWNLSKLNMLKPDSDCLCFAMLCTLHDKCDRLRKAYGEACSG 185
 Db 129 YELDVSPYEDVTGSKPWKWNLSKLNMLKPDSDCLCFAMLCTLHDKCDRLRKAYGEACSG 188
 QY 186 IRCORHLCLAOLRSFFFEKAAESHAQGLLLCPACEDACGERRRNTIAPSCALPSVTENC 245
 Db 189 PHCORHVCLRQLLFFFEKAAEPHAQGLLLCPACNDRCGERRRNTIAPNCALPPVAPNC 248
 QY 246 LDLRSFCRADPLCRSRLMDFQTHCPMDILGTCAEQSRCLRAYLGLIGTAMTNFISKV 305
 Db 249 LELRFLCFSDPLCRSRLVDFQTHCPMDILGTCAEQSRCLRAYLGLIGTAMTNFVSNV 308
 QY 306 NTTVALSCTCRSGNLQDECCEQLERSFSQNPCLVEAIAAKWRFHQLFSQDWADSTFSV 365
 Db 309 NTSVALSCTCRSGNLQDECCEMLEGFFSHNPCLTEATAAKMRFHSQLSQDPWHPPTFAVM 368
 QY 366 QOQNSNPALRQPLRPILSFSILPILLOTW 397
 Db 369 AHQENPAVRPQWPVPSLFSCTLPILLLSLW 400
 RESULT 15
 AAW84186
 ID AAW84186 standard; protein; 400 AA.
 XX AAW84186;
 XX AC AAW84186;
 XX DT 25-MAR-1999 (first entry)
 XX DE Glial cell line-derived neurotrophic factor receptor gamma 2.
 XX KW Glial cell line-derived neurotrophic factor receptor gamma 2;
 KW GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;
 KW neurodegenerative disease; amyotrophic lateral sclerosis; GDNFR-gamma2;
 KW Parkinson's disease; schizophrenia; insomnia; tardive dyskinesia;
 KW hypertension; pituitary adenomas; hyperprolactinemia; thyroid tumour;
 KW renal disorder; kidney failure; gut dysfunction; regeneration;
 KW cardiomyocyte; epithelium; hepatocyte.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FT Peptide 1..31 /label= signal_peptide
 FT Protein 32..400 /label= mature_protein
 FT Domain 32..382 /note= "extracellular domain"
 FT Domain 383..400 /note= "transmembrane domain"
 XX WO9853069-A2.
 XX PD 26-NOV-1998.
 XX PF 20-MAY-1998; 98WO-US010328.
 XX PR 20-MAY-1997; 97US-0047092P.
 XX PR 27-JUN-1997; 97US-00884638.

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 7, 2006, 23:31:14 ; Search time 55.126 Seconds
(without alignments)
3009.073 Million cell updates/sec

Title: US-10-621-855-5

Perfect score: 2131

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2131	100.0	397	3	US-09-220-920-64
2	2131	100.0	397	5	US-10-668-936-17
3	2131	100.0	397	5	US-10-621-855-5
4	1972	92.5	397	5	US-10-872-161-42
5	1880	88.2	888	5	US-10-621-855-20
6	1774	83.2	346	5	US-10-668-936-15
7	1646.5	77.3	400	3	US-09-220-920-63
8	1646.5	77.3	400	3	US-09-828-366-16
9	1646.5	77.3	400	5	US-10-668-936-21
10	1646.5	77.3	400	5	US-10-621-855-15
11	1646.5	77.3	628	5	US-10-621-855-18
12	1643.5	77.1	400	5	US-10-482-029-275
13	1642.5	77.1	400	5	US-10-872-161-38
14	1458	68.4	369	5	US-10-621-855-17
15	1386	65.0	315	5	US-10-668-936-19
16	654	30.7	498	5	US-10-872-161-43
17	640.5	30.1	489	5	US-10-872-161-44
18	577.5	27.1	445	4	US-10-673-007-11
19	577.5	27.1	460	5	US-10-872-161-40
20	577.5	27.1	464	3	US-09-388-316-6
21	577.5	27.1	464	4	US-10-357-822-6
22	577.5	27.1	464	4	US-10-673-007-2
23	577.5	27.1	464	5	US-10-621-855-9
24	577.5	27.1	664	3	US-09-388-316-18
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26	577.5	27.1	951	5	US-10-621-855-19
27	574.5	27.0	464	3	US-09-388-316-3

28	574.5	27.0	464	4	US-10-357-822-3	Sequence 3, Appli
29	574.5	27.0	464	4	US-10-673-007-9	Sequence 9, Appli
30	574.5	27.0	464	5	US-10-872-161-36	Sequence 36, Appli
31	574.5	27.0	464	5	US-10-723-850-3950	Sequence 3950, Ap
32	574.5	27.0	464	5	US-10-668-936-13	Sequence 13, Appli
33	574.5	27.0	464	5	US-10-621-855-7	Sequence 7, Appli
34	574.5	27.0	664	3	US-09-388-316-16	Sequence 16, Appli
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36	515	24.2	460	4	US-10-241-220-62	Sequence 62, Appli
37	515	24.2	460	5	US-10-872-972-62	Sequence 62, Appli
38	515	24.2	460	5	US-10-872-931-62	Sequence 62, Appli
39	515	24.2	460	5	US-10-668-936-11	Sequence 11, Appli
40	515	24.2	460	5	US-10-621-855-6	Sequence 6, Appli
41	513.5	24.1	463	4	US-10-155-693-10	Sequence 10, Appli
42	513.5	24.1	463	4	US-10-155-693-12	Sequence 12, Appli
43	513.5	24.1	463	5	US-10-872-161-10	Sequence 10, Appli
44	513.5	24.1	463	5	US-10-872-161-12	Sequence 12, Appli
45	513.5	24.1	465	4	US-10-357-822-22	Sequence 22, Appli

ALIGNMENTS

RESULT 1

US-09-220-920-64

; Sequence 64, Application US/09220920

; Patent No. US2002002269A1

; GENERAL INFORMATION:

; APPLICANT: Milbrandt, Jeffrey D.

; APPLICANT: Baloh, Robert H.

; TITLE OF INVENTION: Artemin, A No. US2002002269A1e1 Neurotrophic Factor

; FILE REFERENCE: 6029-7996

; CURRENT APPLICATION NUMBER: US/09/220,920

; CURRENT FILING DATE: 1998-12-24

; EARLIER APPLICATION NUMBER: 09/163,283

; EARLIER FILING DATE: 1998-09-29

; EARLIER APPLICATION NUMBER: 60/108,148

; EARLIER FILING DATE: 1998-11-12

; EARLIER APPLICATION NUMBER: 09/218,698

; EARLIER FILING DATE: 1998-12-22

; NUMBER OF SEQ ID NOS: 120

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 64

; LENGTH: 397

; TYPE: PRT

; ORGANISM: Murine

US-09-220-920-64

Query Match 100.0%; Score 2131; DB 3; Length 397;

Best Local Similarity 100.0%; Pred. No. 2.6e-182;

Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGLSWSPRPPLMLILLVLSLWLP	AGNSLATENRFVNSCTQARKCEANPAC	QYH 60
Db	1	MGLSWSPRPPLMLILLVLSLWLP	AGNSLATENRFVNSCTQARKCEANPAC	QYH 60
Qy	61	LGSCSTSLSPPLLESAMADCLAEAO	LNLSIDCRCHRRMKHQATCLDIYVTH	HPA 120
Db	61	LGSCSTSLSPPLLESAMADCLAEAO	LNLSIDCRCHRRMKHQATCLDIYVTH	HPA 120
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Qy	181	EACSGICQSHLCQAOLRSFFEXAA	SHQAOLGLLCCPACEDAGCGERRNT	IAPSCALPS 240
Db	181	EACSGICQSHLCQAOLRSFFEXAA	SHQAOLGLLCCPACEDAGCGERRNT	IAPSCALPS 240
Qy	241	VTNCLDLRSFCRADPLCRSLRMD	FQTHCHPMIDILGTCAEQSRCLP	AYLGLIGTAMTPN 300
Db	241	VTNCLDLRSFCRADPLCRSLRMD	FQTHCHPMIDILGTCAEQSRCLP	AYLGLIGTAMTPN 300
Qy	301	FISKVNTVALSCTCRSGNLDCEQ	LSRFSFQNPCLVEAIAAKMFRH	QLFSQDWADS 360

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Db 301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRHRLQFSQDWADS 360
Qy 361 TFSVVQQNSNPALRLOPRLPILSILPLILLQTLW 397
Db 361 TFSVVQQNSNPALRLOPRLPILSILPLILLQTLW 397

RESULT 2
US-10-668-936-17
; Sequence 17, Application US/10668936
; Publication No. US20050080235A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/668,936
; FILING DATE: 23-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/187,906
; FILING DATE: 06-NOV-1998
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-668-936-17

Query Match 100.0%; Score 2131; DB 5; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.6e-182;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 LGSCTSSLSRPLPLEESAMSADCLEAAEQRLNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120
Db 61 LGSCTSSLSRPLPLEESAMSADCLEAAEQRLNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120

Qy 121 RSLGDYELDVSPYEDTVTSKPKWKNLSKLNMLKPDSDILCLKFAMLCCTLHDKCDRLRKAYG 180
Db 121 RSLGDYELDVSPYEDTVTSKPKWKNLSKLNMLKPDSDILCLKFAMLCCTLHDKCDRLRKAYG 180

Query Match 100.0%; Score 2131; DB 5; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.6e-182;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 181 EACSGIRCORHLCLAQLRSFFFEKAAESHAQGLLLCPCAPEDAGCGGERRRNTIAPSCALPS 240
Db 181 EACSGIRCORHLCLAQLRSFFFEKAAESHAQGLLLCPCAPEDAGCGGERRRNTIAPSCALPS 240
Qy 241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMIDILGTCTATEQSRCRLAYLGLIGTAMTPN 300
Db 241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMIDILGTCTATEQSRCRLAYLGLIGTAMTPN 300
Qy 301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRHRLQFSQDWADS 360
Db 301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRHRLQFSQDWADS 360
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Db 361 TFSVVQQNSNPALRLOPRLPILSILPLILLQTLW 397

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RESULT 3
US-10-621-855-5
; Sequence 5, Application US/10621855
; Publication No. US20050221330A1
; GENERAL INFORMATION:
; APPLICANT: De Sauvage, Frederic J.
; APPLICANT: Klein, Richard D.
; APPLICANT: Rosenthal, Arnon
; APPLICANT: Phillips, Heidi S.
; TITLE OF INVENTION: GFRALPHA3 AND ITS USES
; FILE REFERENCE: GENENT.065A
; CURRENT APPLICATION NUMBER: US/10/621,855
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 09/272,835
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 60/079,124
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 60/081,569
; PRIOR FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-621-855-5

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Query Match 100.0%; Score 2131; DB 5; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.6e-182;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSWSRPPLMLILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACAAAYQH 60
Db 1 MGLSWSRPPLMLILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACAAAYQH 60

Qy 61 LGSCTSSLSRPLPLEESAMSADCLEAAEQRLNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120
Db 61 LGSCTSSLSRPLPLEESAMSADCLEAAEQRLNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120

Qy 121 RSLGDYELDVSPYEDTVTSKPKWKNLSKLNMLKPDSDILCLKFAMLCCTLHDKCDRLRKAYG 180
Db 121 RSLGDYELDVSPYEDTVTSKPKWKNLSKLNMLKPDSDILCLKFAMLCCTLHDKCDRLRKAYG 180
Qy 181 EACSGIRCORHLCLAQLRSFFFEKAAESHAQGLLLCPCAPEDAGCGGERRRNTIAPSCALPS 240
Db 181 EACSGIRCORHLCLAQLRSFFFEKAAESHAQGLLLCPCAPEDAGCGGERRRNTIAPSCALPS 240
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Db 241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMIDILGTCTATEQSRCRLAYLGLIGTAMTPN 300

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Qy 301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEIAAKMRHRLQFSQDWADS 360
 Db 301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEIAAKMRHRLQFSQDWADS 360
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 Db 361 TFSVVOQNSNPALRQLRPLTSLPILILLQTLW 397

RESULT 4
 US-10-872-161-42
 ; Sequence 42, Application US/10872161
 ; Publication No. US20040235714A1
 ; GENERAL INFORMATION:
 ; APPLICANT: De Sauvage, Frederic J.
 ; APPLICANT: Klein, Richard D.
 ; APPLICANT: Rosenchal, Arnon
 ; APPLICANT: Phillips, Heidi S.
 ; TITLE OF INVENTION: GFRALPHA3 AND ITS USES
 ; FILE REFERENCE: GENENT.065A
 ; CURRENT APPLICATION NUMBER: US/10/621,855
 ; CURRENT FILING DATE: 2003-07-16
 ; PRIOR APPLICATION NUMBER: 09/272,835
 ; PRIOR FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: 60/079,124
 ; PRIOR FILING DATE: 1998-03-23
 ; PRIOR APPLICATION NUMBER: 60/081,569
 ; PRIOR FILING DATE: 1998-04-13
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 888
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Chimeric receptor comprising murine sequence.
 ; US-10-621-855-20

Query Match 92.5%; Score 1972; DB 5; Length 397;
 Best Local Similarity 92.9%; Pred. No. 4.6e-168;
 Matches 369; Conservative 9; Mismatches 19; Indels 0; Gaps 0;
 Qy 1 MGLSWSRPPPLMTILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACAAAYQH 60
 Db 1 MGLSRSRPPPLVILLVLSLWPLGTNSLPTENRLVNSCTQARKKCEANPACAAAYQH 60
 Qy 61 LGSCTSSLSRPLPLEESAMSDCLAEAEQLRNSLIDCRCHRRMKHQATCLDIYVTVHPA 120
 Db 61 LDSCTPSLSPGEGATSAAQLEAQLRNSLIDCRCHRRMKHQATCLDIYVTVHPV 120
 Qy 121 RSLGDELVSYPEDTTSKPKWKNLSKLNMLKPDSDCLCKFAMLCITLHDKCDRLRKAYG 180
 Db 121 RSLGDELVSYPEDTTSKPKWKNLSKLNMLKPDSDCLCKFAMLCITLHDKCDRLRKAYG 180
 Qy 181 EACSGIRCORHLCIAQLRSFPEKAESHAQGLLLCPCAPEDAGGERRRNTIAPSCALPS 240
 Db 181 EACSGIRCORHLCIAQLRSFPEKAESHAQGLLLCPCAPEDAGGERRRNTIAPSCALPS 240
 Qy 241 VTPNCLDRSFCRADPLCRSLRMDFOTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPN 300
 Db 241 VAPNCLDRSFCRADPLCRSLRMDFOTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPN 300
 Qy 301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEIAAKMRHRLQFSQDWADS 360
 Db 301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEIAAKMRHRLQFSQDWADS 360
 Qy 361 TFSVVOQNSNPALRQLRPLTSLPILILLQTLW 397
 Db 361 TFSVVOQNSNPALRQLRPLTSLPILILLQTLW 397

RESULT 5
 US-10-621-855-20
 ; Sequence 20, Application US/10621855

Publication No. US20050221330A1
 ; GENERAL INFORMATION:
 ; APPLICANT: De Sauvage, Frederic J.
 ; APPLICANT: Klein, Richard D.
 ; APPLICANT: Rosenchal, Arnon
 ; APPLICANT: Phillips, Heidi S.
 ; TITLE OF INVENTION: GFRALPHA3 AND ITS USES
 ; FILE REFERENCE: GENENT.065A
 ; CURRENT APPLICATION NUMBER: US/10/621,855
 ; CURRENT FILING DATE: 2003-07-16
 ; PRIOR APPLICATION NUMBER: 09/272,835
 ; PRIOR FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: 60/079,124
 ; PRIOR FILING DATE: 1998-03-23
 ; PRIOR APPLICATION NUMBER: 60/081,569
 ; PRIOR FILING DATE: 1998-04-13
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 888
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Chimeric receptor comprising murine sequence.
 ; US-10-621-855-20

Query Match 88.2%; Score 1880; DB 5; Length 888;
 Best Local Similarity 94.1%; Pred. No. 2.2e-159;
 Matches 354; Conservative 5; Mismatches 11; Indels 6; Gaps 1;
 Qy 25 LGAGNSLATENRFVNSCTQARKKCEANPACAAAYQHLSGCTSSLSRPLPLEESAMSDCL 84
 Db 54 LEAGNSLATENRFVNSCTQARKKCEANPACAAAYQHLSGCTSSLSRPLPLEESAMSDCL 113
 Qy 85 EAAEQLRNSLIDCRCHRRMKHQATCLDIYVTVHPARSLGDELVSYPEDTTSKPKWM 144
 Db 114 EAAEQLRNSLIDCRCHRRMKHQATCLDIYVTVHPARSLGDELVSYPEDTTSKPKWM 173
 Qy 145 NLSKLNMLKPDSDCLCKFAMLCITLHDKCDRLRKAYGACSGIRCORHLCIAQLRSFPEKA 204
 Db 174 NLSKLNMLKPDSDCLCKFAMLCITLHDKCDRLRKAYGACSGIRCORHLCIAQLRSFPEKA 233
 Qy 205 AESHAQGLLLCPCAPEDAGGERRRNTIAPSCALPSVTPNCLDRSFCRADPLCRSLMD 264
 Db 234 AESHAQGLLLCPCAPEDAGGERRRNTIAPSCALPSVTPNCLDRSFCRADPLCRSLMD 293
 Qy 265 FQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFISKVNTTVALSCTCRGSGNLQDE 324
 Db 294 FQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFISKVNTTVALSCTCRGSGNLQDE 353
 Qy 325 CEQLERSFSQNPCLVEIAAKMRHRLQFSQDWADSTFSVVOQNSNPALR-----LQP 378
 Db 354 CEQLERSFSQNPCLVEIAAKMRHRLQFSQDWADSTFSVVOQNSNPALR-----LQP 413
 Qy 379 RLPILSFSILPILLQ 394
 Db 414 LTALVTAAALALILR 429

RESULT 6
 US-10-668-936-15
 ; Sequence 15, Application US/10668936
 ; Publication No. US20050080235A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BIOGEN, INC.
 ; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural and Renal Growth
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Biogen, Inc.
 ; STREET: 14 Cambridge Center
 ; CITY: Cambridge
 ; STATE: MA

COUNTRY: USA
ZIP: 02142
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/10/668,936
APPLICATION NUMBER: US/10/668,936
FILING DATE: 23-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/187,906
FILING DATE: 08-NOV-1998
APPLICATION NUMBER: PCT/US97/07726
FILING DATE: 07-MAY-97
APPLICATION NUMBER: US 60/017,427
FILING DATE: 08-MAY-96
APPLICATION NUMBER: US 60/019,300
FILING DATE: 07-JUN-96
APPLICATION NUMBER: US 60/021,859
FILING DATE: 16-JUL-96
APPLICATION NUMBER: US 60/043,533
FILING DATE: 10-APR-97
ATTORNEY/AGENT INFORMATION:
NAME: Kaplan, Warren A.
REGISTRATION NUMBER: 34,199
REFERENCE/DOCKET NUMBER: A008 PCT CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-679-2400
TELEFAX: 617-679-2838
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-668-936-15

Query Match 83.2%; Score 1774; DB 5; Length 346;
Best Local Similarity 100.0%; Pred. No. 2.2e-150;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 68 LSRPLPLEESAMSDCLEAAEQLRNSSLIDCRRMKHQATCLDIYWTVHPARSLGDYE 127
DB 17 LSRPLPLEESAMSDCLEAAEQLRNSSLIDCRRMKHQATCLDIYWTVHPARSLGDYE 76
QY 128 LDVSPYEDTTSKPKMNLKLNMLKPSDCLCKFAMLCITLHDKCDRLRKAYGEACSGIR 187
DB 77 LDVSPYEDTTSKPKMNLKLNMLKPSDCLCKFAMLCITLHDKCDRLRKAYGEACSGIR 136
QY 188 CORHLCLAQLRFFFEKAAESHAQGLLLCPADEDAGCGERRRNTIAPSCALPSVTPNCLD 247
DB 137 CORHLCLAQLRFFFEKAAESHAQGLLLCPADEDAGCGERRRNTIAPSCALPSVTPNCLD 196
QY 248 LRSFCRADPLCRSLRMDFTQCHPMDILGTCAEQSRCLRAYLIGLTAMTNPFIKSVKNT 307
DB 197 LRSFCRADPLCRSLRMDFTQCHPMDILGTCAEQSRCLRAYLIGLTAMTNPFIKSVKNT 256
QY 308 TVALSCTCRGSGNLQDECEQLERSFQNPCLVEATAAKMRFHRLQFSQDWDSTFSVVOQ 367
DB 257 TVALSCTCRGSGNLQDECEQLERSFQNPCLVEATAAKMRFHRLQFSQDWDSTFSVVOQ 316
QY 368 QNSNPALRLQPLPILSFLPILILLQTLW 397
DB 317 QNSNPALRLQPLPILSFLPILILLQTLW 346

RESULT 7
US-09-220-920-63
; Sequence 63, Application US/09220920
; Patent No. US20020002269A1

GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
; APPLICANT: Baloh, Robert H.
; TITLE OF INVENTION: Artemin, A No. US20020002269A1el Neurotrophic Factor
; FILE REFERENCE: 6029-7996
; CURRENT APPLICATION NUMBER: US/09/220,920
; CURRENT FILING DATE: 1998-12-24
; EARLIER FILING DATE: 1998-09-29
; EARLIER FILING DATE: 1998-11-12
; EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-220-920-63
Query Match 77.3%; Score 1646.5; DB 3; Length 400;
Best Local Similarity 77.8%; Pred. No. 7.2e-139;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;
QY 7 PRPP-LMILLVLSLWPLGAGNSLATENFVNSCTQARKKCEANPACKAAYQHLSGCT 65
DB 9 PLPPVLMILLVLSLWPLGAGNSLATENFVNSCTQARKKCEANPACKAAYQHLSGCT 68
QY 66 SLSRPLPLEESAMSDCLEAAEQLRNSSLIDCRRMKHQATCLDIYWTVHPARSLGD 125
DB 69 SLSRPLPLEESAMSDCLEAAEQLRNSSLIDCRRMKHQATCLDIYWTVHPARSLGD 128
QY 126 YELDVSPYEDTTSKPKMNLKLNMLKPSDCLCKFAMLCITLHDKCDRLRKAYGEACSG 185
DB 129 YELDVSPYEDTTSKPKMNLKLNMLKPSDCLCKFAMLCITLHDKCDRLRKAYGEACSG 188
QY 186 IRCORHLCLAQLRFFFEKAAESHAQGLLLCPADEDAGCGERRRNTIAPSCALPSVTPNC 245
DB 189 PHCORHLCLAQLRFFFEKAAESHAQGLLLCPADEDAGCGERRRNTIAPSCALPSVTPNC 248
QY 246 LDLSFCRADPLCRSLRMDFTQCHPMDILGTCAEQSRCLRAYLIGLTAMTNPFIKSV 305
DB 249 LELARLCLAQLRFFFEKAAESHAQGLLLCPADEDAGCGERRRNTIAPSCALPSVTPNC 308
QY 306 NTVALSCTCRGSGNLQDECEQLERSFQNPCLVEATAAKMRFHRLQFSQDWDSTFSV 365
DB 309 NTVALSCTCRGSGNLQDECEQLERSFQNPCLVEATAAKMRFHRLQFSQDWDSTFSV 368
QY 366 QNSNPALRLQPLPILSFLPILILLQTLW 397
DB 369 AHQNPALRPQPVVPSLFSCTPLILLSLW 400

RESULT 8
US-09-828-366-16
; Sequence 16, Application US/09828366
; Patent No. US20020010137A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Klein, Robert D.
; APPLICANT: Napier, Mary
; APPLICANT: Wood, William I.
; APPLICANT: Yuan, Jean
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
; FILE REFERENCE: P1694R1C1
; CURRENT APPLICATION NUMBER: US/09/828,366
; CURRENT FILING DATE: 2001-04-05
; Prior filing data removed - refer to PALM or file wrapper

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 7, 2006, 23:31:54 ; Search time 6.94866 Seconds
(without alignments)
1142.691 Million cell updates/sec

Title: US-10-621-855-5

Perfect score: 2131

Sequence: 1 MGLSWSPRLPMLILLVLS.....PRLPILSPILPILLQLTLW 397

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 135346 seqs, 20000420 residues

Total number of hits satisfying chosen parameters: 135346

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.New.*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
- 4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
- 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pap.*
- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pap.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	132	6.2	4544	7 US-11-076-427A-32	Sequence 32, Appl
2	123	5.8	1170	7 US-11-114-962-5	Sequence 5, Appl
3	118.5	5.6	2556	7 US-11-050-346-67	Sequence 67, Appl
4	114.5	5.4	1433	7 US-11-114-962-1	Sequence 1, Appl
5	108.5	5.1	1268	6 US-10-453-372-1144	Sequence 1144, Ap
6	108.5	5.1	1268	6 US-10-453-372-1154	Sequence 1154, Ap
7	108.5	5.1	1288	6 US-10-453-372-1152	Sequence 1152, Ap
8	108.5	5.1	1288	6 US-10-453-372-1152	Sequence 1152, Ap
9	108	5.0	1400	6 US-10-821-234-1045	Sequence 1045, Ap
10	106	5.0	2911	7 US-11-090-617-706	Sequence 706, App
11	105.5	5.0	401	7 US-11-072-175-224	Sequence 224, App
12	104	4.9	1193	7 US-11-022-478-8	Sequence 8, Appl
13	103	4.8	1379	7 US-11-114-962-4	Sequence 4, Appl
14	102	4.8	999	7 US-11-113-424-36	Sequence 36, Appl
15	102	4.8	1218	7 US-11-078-735-20	Sequence 20, Appl
16	102	4.8	1218	7 US-11-050-346-65	Sequence 65, Appl
17	102	4.8	1218	7 US-11-103-077-20	Sequence 20, Appl
18	102	4.8	1218	7 US-11-072-175-155	Sequence 155, App
19	102	4.8	1218	7 US-11-022-478-4	Sequence 4, Appl
20	101	4.7	997	7 US-11-080-991-50	Sequence 50, Appl
21	100	4.7	728	7 US-11-022-478-11	Sequence 11, Appl
22	100	4.7	969	6 US-10-055-877-214	Sequence 214, App
23	100	4.7	1620	6 US-10-453-372-868	Sequence 868, App
24	99.5	4.7	712	7 US-11-050-857-952	Sequence 952, App
25	99.5	4.7	806	7 US-11-050-857-951	Sequence 951, App

ALIGNMENTS

RESULT 1

US-11-076-427A-32
; Sequence 32, Application US/11076427A
; Publication No. US20060025338A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, et al.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF LYMPHATIC AND VENOUS
; FILE REFERENCE: 28967/40008A
; CURRENT APPLICATION NUMBER: US/11/076.427A
; PRIOR FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US 60/551,581
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 32
; LENGTH: 4544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-076-427A-32

Query Match	6.2%	Score 132;	DB 7;	Length 4544;
Best Local Similarity	20.2%;	Pred. No. 0.0011;		
Matches	78;	Conservative	35;	Mismatches 142;
				Indels 132;
				Gaps 20;
Qy	62	GSCTSSLSRPLPLEESAMSDCLEAARLNSSLIIDCRCHRM-----KHQATCL	111	
Db	2615	GTCTGNSR-----CNQFVDCEDASDEM-NCSATDCSSYFRLGVGVLPQCERTSLCY	2667	
Qy	112	DIYVTHVPARSLGVDLYSPYEDTVTSKPMKNLKLMLKPSDLCLKFAMLTCLHDK	171	
Db	2668	APSWCVDGANDCGD-----YSERDCPGVKRPRCPPLNVFACPSGRCPMSWTCDKDD	2720	
Qy	172	CDRLRKAYGE-----ACS--GIRCORHLCLAO-----LRSFEEKAESHAQG--	211	
Db	2721	CE-----HGEDETHCNKFCSEAOFEQCNHRCISQKWLCDGSDGDCGDSDEAA--HCEGKT	2773	
Qy	212	-----LLLCP-----CAPE-----DAGGERRRNTIAPSCALPSVTPN-----CLDL	248	
Db	2774	CGPSSFCPGTHVCPVPRWLCDGDKDCADGADEIAAGCLYNSTCDDREFMCONRQIPK	2833	
Qy	249	RSFCRAD-----PLC-----RSRLMDFQTHCHPMDLGT--	277	
Db	2834	HFVCDHRDRCADGSDSECEPYPTCGSEFRANCGRCLSSRQWECDCGENDCHQDSEAPK	2893	
Qy	278	---CATSQSRLRAYLGLIGTAMTPNFIKVNITVALSCTCRGSGNQLQDEC--EQLERSF	332	
Db	2894	NPHCTSPHKC-----NASSQFLCSSGRCAEALLCNG-----QDDCGDSSDERGC	2939	

QY 333 SONPCLVEAIAAKRPHROLFSQDWAD 359
Db 2940 HINECLSRKLSG-----CSQDCED 2958

RESULT 2
US-11-114-962-5
; Sequence 5, Application US/11114962
; Publication No. US20060030694A1
; GENERAL INFORMATION:
; APPLICANT: Kitajewski, Jan
; APPLICANT: Shawber, Carrie
; APPLICANT: Funahashi, Yasuhiro
; TITLE OF INVENTION: Notch-Based Fusion Proteins And Uses Thereof
; FILE REFERENCE: 0575/71308-A
; CURRENT APPLICATION NUMBER: US/11/114,962
; CURRENT FILING DATE: 2005-04-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 1170
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-114-962-5

Query Match 5.8%; Score 123; DB 7; Length 1170;
Best Local Similarity 22.6%; Pred. No. 0.0015;
Matches 81; Conservative 33; Mismatches 156; Indels 88; Gaps 19;

QY 40 SCTQARKKEAMP-----ACKAAYOHLG-SCTSSLSRPLPLESAMSDCL 84
Db 722 TCSEEVTACHSGFLNGSGCSIRPEGYSCITLPSHTGRHCQTAV-----DHCVSASCL 774
QY 85 EA-----ABQLRNSSLIDCRCHRRMKHOATCLDIYVTHPARS 122
Db 775 NGTCVNKGSTFCLCATGFOGLHCEKTNPCASDPC-----RNKATCOD---TRGARC 827
QY 123 L---GDYELDVSPYEDTVTSKPKWNLSKLNMLKPDSDI,CLK--FAMLTCLHDKCDRLRK 177
Db 828 LCSPGYTGSSCQTLDLCARKPCPHARCLOSGPSFQCLCQGWTCALCDFPLSCQKAAM 887
QY 178 ANGEACSGTRCQR-HLCLLAQLSRFFFEKAESAHAQGLL-----LCPCAPEDAGGERRNTI 232
Db 888 SOGIEISGL-CONGGICIDTSGSYFCRCPPGF-QGKLQODNVNCPENPCHHG---STC 941
QY 233 AP-----SCALPSVTPNCLDIRSFCRADP-----LCRSRLMDFQTHCHPMDILGTAT 280
Db 942 VPQPSGVVCCAPGYEGQNSKVLDACQSQPCPNHGTCTSRPGGFHCACFPFGVGLRCBG 1001
QY 281 EOSRCLRAYLGLIGTAMTNPFTSKVNTVALSCTCRGNSNLODECEQLERSFSQN-PC 337
Db 1002 DVDECLDRPCPSGTAACHSLAN-----AFYCOQL-PGHTGORCE-VEMDLQSQOPC 1051

RESULT 3
US-11-050-346-67
; Sequence 67, Application US/11050346
; Publication No. US20060002924A1
; GENERAL INFORMATION:
; APPLICANT: BODMER, MARK WILLIAM
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: TUGAL, TAMARA
; APPLICANT: WARD, GEORGE ALBERT
; TITLE OF INVENTION: CONJUGATE OF NOTCH SIGNALLING PATHWAY MODULATORS AND
; FILE REFERENCE: 674525-2016
; CURRENT APPLICATION NUMBER: US/11/050,346
; CURRENT FILING DATE: 2005-02-03
; PRIOR APPLICATION NUMBER: GB 0312062.3
; PRIOR FILING DATE: 2003-05-24

; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: GB 0218068.5
; PRIOR FILING DATE: 2002-08-03
; PRIOR APPLICATION NUMBER: GB 0220849.4
; PRIOR FILING DATE: 2002-09-07
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 67
; LENGTH: 2556
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (891)
; OTHER INFORMATION: Variable amino acid
US-11-050-346-67

Query Match 5.6%; Score 118.5; DB 7; Length 2556;
Best Local Similarity 20.1%; Pred. No. 0.01;
Matches 84; Conservative 48; Mismatches 135; Indels 151; Gaps 26;

QY 39 NSCTQARKKCBANPACAAAYOHLGSCSTSLRPL---PLESAMSD-CLEAAEQLRNSS 94
Db 379 NPCNEG-SNCDTNPVNGKA---ICTCPSGYTGPAQSDVDDECSLGNAPCEHAGKICINTLG 434
QY 95 LIDCEC-----HRRMKHOATCLDIYVTHPARSLGDYELDVSP-YE-- 134
Db 435 SFEQCQLOGYTGPRCEIDVNECVSNPCQNDATCLD-----QIGBFQCMCPGYEGV 485
QY 135 -----DVTVTSKPKWN---LSKLN-----MLKPDSDI,CLK----- 161
Db 486 HCEVNTDECAASPCLHNGRCLDKINEFOCECPTGTGHLCOYDVDECASTPCNGAKCLD 545
QY 162 ----FAMLTCT-----LH-----DKDLRLKAYGEACSGIRCOHCLLAQLSRFFFEKAARS 207
Db 546 GPNTYTCVCTEGYTGTHCEVDIDECDPDPCHYGCKDGVATFTCLCRP---GYTGHHCET 602
QY 208 HAQGLLLCPCA-----PEDAGCGERRNTIAPSCAL-----PSVTPNCLD-LRSF 251
Db 603 NINECSSOPCLRGTGCPQDPDNAYLCFLUKGTTGPNCEINLDDCASSPCDSGTCLDKIDGY 662
QY 252 -CRADP-----LCRSRLMDFQTH-CHPMDILGTATE-----QSRCLRAYLGLIGTAMTPN 300
Db 663 ECACEPGYTGSMCNNSNIDEACAGNCPCHG---GTCEDGINGFTCRCEGY-----HDTPT 712
QY 301 FISKVNTVALSC---TCRGSN-----LODECEQLERSFSQNPLC 338
Db 713 CLSEVNECNPNVHGACRDSLNGYKCDPCDPSGNTNCDINNECE-----SNPCV 763

RESULT 4
US-11-114-962-1
; Sequence 1, Application US/11114962
; Publication No. US20060030694A1
; GENERAL INFORMATION:
; APPLICANT: Kitajewski, Jan
; APPLICANT: Shawber, Carrie
; APPLICANT: Funahashi, Yasuhiro
; TITLE OF INVENTION: Notch-Based Fusion Proteins And Uses Thereof
; FILE REFERENCE: 0575/71308-A
; CURRENT APPLICATION NUMBER: US/11/114,962
; CURRENT FILING DATE: 2005-04-26

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 7, 2006, 23:30:09 ; Search time 14.3606 Seconds
(without alignments)
2659.928 Million cell updates/sec

Title: US-10-621-855-5
Perfect score: 2131
Sequence: 1 MGLSWSPRPPLMLLLVLS.....PRLPILSFLPILLOTLW 397

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2131	100.0	397	2 JE0082	GPI-linked recepto
2	132	6.2	4544	1 S02392	alpha-2-macroglobu
3	131	6.1	4545	1 S25111	alpha-2-macroglobu
4	124	5.8	1722	2 E89753	protein Filic7.4 [1
5	123	5.8	1964	2 T09059	notch4 - mouse
6	120.5	5.7	2531	2 A46019	notch-1 protein -
7	118	5.5	2555	2 A40043	notch protein homo
8	117	5.5	1746	1 S19694	tenascin precursor
9	117	5.5	4543	1 A33102	alpha-2-macroglobu
10	114.5	5.4	2531	2 S18188	notch protein homo
11	114	5.3	2437	2 S42612	transmembrane prot
12	112.5	5.3	2703	1 A24420	notch protein - fr
13	110	5.2	965	2 S62935	hypothetical prote
14	110	5.2	1187	2 T18355	hypothetical prote
15	110	5.2	2321	2 S78549	notch3 protein - h
16	109.5	5.1	2233	2 T28669	surface protein 51
17	109	5.1	1047	2 D71302	probable exonuclea
18	108	5.1	1394	2 A35626	transforming growt
19	108	5.1	1712	2 A38261	masking protein pr
20	108	5.1	1847	2 T18308	probable vitellog
21	107.5	5.0	996	2 JE0237	apolipoprotein E r
22	107.5	5.0	2150	2 T32497	hypothetical prote
23	107	5.0	3051	2 S42373	hypothetical prote
24	106.5	5.0	2019	1 J01322	tenascin precursor
25	106	5.0	2918	2 A54105	fibrillin-2 precu
26	105.5	5.0	384	2 S25771	gas1 protein - mou
27	105.5	5.0	873	1 A49729	VLDL receptor prec
28	105	4.9	1077	2 T41146	probable cysteine-
29	105	4.9	1106	2 T13938	gene shuttle craft

30	105	4.9	1408	2 S16148	gene serrate prote
31	104.5	4.9	1203	2 A49175	Notch B protein -
32	103.5	4.9	869	1 JC4858	VLDL receptor prec
33	103	4.8	886	2 A57172	probable hormone r
34	103	4.8	2318	2 S45306	notch 3 protein -
35	102.5	4.8	835	2 JP0076	notch 3 protein -
36	102.5	4.8	1188	2 D86236	protein Fl4N23.5 [
37	102	4.8	1220	2 A56136	jagged protein pre
38	101.5	4.8	593	1 GYHU	granulin precursor
39	100.5	4.7	5376	2 T42215	zonadhesin - mouse
40	100	4.7	728	2 I50719	C-Delta-1 - chicke
41	100	4.7	1106	2 T44598	hypothetical prote
42	99.5	4.7	2471	2 A49128	cell-fate determin
43	99.5	4.7	2718	2 A23475	G surface protein
44	99	4.6	2704	2 S09118	G surface protein
45	99	4.6	2907	2 A57278	fibrillin-2 precu

ALIGNMENTS

RESULT 1

JE0082

GPI-linked receptor precursor - mouse

N:Alternate names: GFRalpha-3

C:Species: Mus musculus (house mouse)

C>Date: 21-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004

C:Accession: JE0082

R:Nomoto, S.; Ito, S.; Yang, L.X.; Kiuchi, K.

Biochem. Biophys. Res. Commun. 244, 849-853, 1998

A:Title: Molecular cloning and expression analysis of GFRalpha-3, a novel cDNA related to

A:Reference number: JE0082; MUID:98205811; PMID:9535755

A:Accession: JE0082

A:Molecule type: mRNA

A:Residues: 1-397 <NOM>

A:Cross-references: UNIPROT:O35118; UNIPARC:UPI000002231A; DBJ:AB008833; NID:G2627159;

C:Comment: This protein plays a distinct role in cell survival and differentiation.

C:Superfamily: Mus musculus GPI-linked receptor

C:Keywords: glycoprotein

F:1-25/Domain: signal sequence #status predicted <SIG>

F:380-397/Region: hydrophobic

F:192,145,306/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	100.0%	Score	2131	DB 2:	Length	397;	
Best Local Similarity	100.0%	Pred. No.	8.2e-166;				
Matches	397;	Conservative	0;	Mismatches	0;	Gaps	0;

Qy	1	MGLSWSPRPPLMLLLVLSLWPLGAGNSLATENRFVNSCTQARKKEANPACAAQYQH	60
Db	1	MGLSWSPRPPLMLLLVLSLWPLGAGNSLATENRFVNSCTQARKKEANPACAAQYQH	60
Qy	61	LGSCTSSLSRPLPLEESAMSDCLAEAEOLNSSLIDCRCHRRMKHQTCLDIYTVHPA	120
Db	61	LGSCTSSLSRPLPLEESAMSDCLAEAEOLNSSLIDCRCHRRMKHQTCLDIYTVHPA	120
Qy	121	RLSGDYELDVSPYEDTVTSKPWNLSKLNMLKPSDLCLKFAMLCTLHDKCDRLRKAYG	180
Db	121	RLSGDYELDVSPYEDTVTSKPWNLSKLNMLKPSDLCLKFAMLCTLHDKCDRLRKAYG	180
Qy	181	EACSGIRCORHLCLAQLSRFFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS	240
Db	181	EACSGIRCORHLCLAQLSRFFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS	240
Qy	241	VTNCLDLRSFCRADPLCRSLMDPQTHCHPMIDILGTCAEQSLRAYLGLIGTAMTPN	300
Db	241	VTNCLDLRSFCRADPLCRSLMDPQTHCHPMIDILGTCAEQSLRAYLGLIGTAMTPN	300
Qy	301	FISKVNTVALSCTCRSGNQLQDECEOLERSFSQNPCLVEAIAAKMFHROLFSQDWADS	360
Db	301	FISKVNTVALSCTCRSGNQLQDECEOLERSFSQNPCLVEAIAAKMFHROLFSQDWADS	360
Qy	361	TFSVVOQNSNPALRLQPRILPILSFLPILLOTLW	397

Db 361 TSVVQQNSPALRLQPLPILSLPILLOTLM 397

RESULT 2

S02392

alpha-2-macroglobulin receptor precursor - human

N:Alternate names: CD91; LDL receptor-related protein 1; low density lipoprotein receptor

C:Species: Homo sapiens (man)

C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004

C:Accession: S02392; S30027; I37998; A39210; S12538

R:Herz, J.; Hamann, U.; Rogne, S.; Myklebost, O.; Gausepohl, H.; Stanley, K.K.

EMBO J. 7, 4119-4127, 1988

A:Title: Surface location and high affinity for calcium of a 500-kd liver membrane protein

A:Reference number: S02392; PMID:89210795; PMID:3266596

A:Accession: S02392

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-4544 <HER>

A:Cross-references: UNIPROT:Q07954; UNIPARC:UPI0000055B03; EMBL:X13916; NID:G34338; PIDN:R.Kristensen, T.

submitted to the EMBL Data Library, October 1990

A:Reference number: S30027

A:Accession: S30027

A:Molecule type: mRNA

A:Residues: 3275-3864 <KRI>

A:Cross-references: UNIPARC:UPI00001736CD; EMBL:X55077

R:Herz, J.; Kowal, R.C.; Goldstein, J.L.; Brown, M.S.

EMBO J. 9, 1769-1776, 1990

A:Title: Proteolytic processing of the 600 kd low density lipoprotein receptor-related protein

A:Reference number: S12538; PMID:90269210; PMID:2112085

A:Contents: annotation; site of proteolytic cleavage

R:Kutt, H.; Herz, J.; Stanley, K.K.

Biochim. Biophys. Acta 1009, 229-236, 1989

A:Title: Structure of the low-density lipoprotein receptor-related protein (LRP) promotes

A:Reference number: I37998; PMID:90089395; PMID:2597675

A:Accession: I37998

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-11 <RES>

A:Cross-references: UNIPARC:UPI0000000A1E; EMBL:X15424; NID:G34408; PIDN:CAA33464.1; PID:R.Strickland, D.K.; Ashcom, J.D.; Williams, S.; Burgess, W.H.; Migliorini, M.; Argraves, J. Biol. Chem. 265, 17401-17404, 1990

A:Title: Sequence identity between the alpha2-macroglobulin receptor and low density lipoprotein

A:Reference number: A39210; PMID:91009181; PMID:1698775

A:Accession: A39210

A:Status: preliminary

A:Molecule type: protein

A:Residues: 150-166; 234-238, 'X', 240-245, 'X', 247-252; 'G', 686-695; 902-916; 1096-1109; 'S', 1765; UNIPARC:UPI00001736DE; UNIPARC:UPI00001736CF; UNIPARC:UPI00001736D0; 605; UNIPARC:UPI00001736D6; UNIPARC:UPI00001736D7

C:Genes: GDB:LRP1; APR; LRP; A2MR

A:Cross-references: GDB:119694; OMIM:107770

A:Map position: 12q13.1-12q13.3

C:Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associated protein (see PIR:A39875).

C:Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding

C:Keywords: beta-hydroxyaspartic acid; calcium binding; glycoprotein

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-3943/Product: alpha-2-macroglobulin receptor 515K chain #status predicted <515K>

F:27-64/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F:72-108/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F:115-148/Domain: EGF homology <EG1>

F:154-188/Domain: EGF homology <EG2>

F:198-239/Domain: LDL receptor YWTD-containing repeat homology <YW01>

F:240-281/Domain: LDL receptor YWTD-containing repeat homology <YW02>

F:292-334/Domain: LDL receptor YWTD-containing repeat homology <YW03>

F:335-378/Domain: LDL receptor YWTD-containing repeat homology <YW04>

F:379-420/Domain: LDL receptor YWTD-containing repeat homology <YW05>

F:421-468/Domain: LDL receptor YWTD-containing repeat homology <YW06>

F:478-519/Domain: EGF homology <EG3>

F:571-613/Domain: LDL receptor YWTD-containing repeat homology <YW07>

F:614-659/Domain: LDL receptor YWTD-containing repeat homology <YW08>

F:660-710/Domain: LDL receptor YWTD-containing repeat homology <YW09>

F:711-752/Domain: LDL receptor YWTD-containing repeat homology <YW10>

F:753-799/Domain: LDL receptor YWTD-containing repeat homology <YW11>

F:807-842/Domain: EGF homology <EG4>

F:854-890/Domain: LDL receptor ligand-binding repeat homology <LDL3>

F:895-931/Domain: LDL receptor ligand-binding repeat homology <LDL4>

F:936-971/Domain: LDL receptor ligand-binding repeat homology <LDL5>

F:976-1011/Domain: LDL receptor ligand-binding repeat homology <LDL6>

F:1015-1051/Domain: LDL receptor ligand-binding repeat homology <LDL7>

F:1062-1097/Domain: LDL receptor ligand-binding repeat homology <LDL8>

F:1104-1140/Domain: LDL receptor ligand-binding repeat homology <LDL9>

F:1145-1182/Domain: LDL receptor ligand-binding repeat homology <LDL10>

F:1185-1221/Domain: EGF homology <EG5>

F:1227-1261/Domain: EGF homology <EG6>

F:1269-1308/Domain: LDL receptor YWTD-containing repeat homology <YW12>

F:1309-1355/Domain: LDL receptor YWTD-containing repeat homology <YW13>

F:1356-1398/Domain: LDL receptor YWTD-containing repeat homology <YW14>

F:1399-1445/Domain: LDL receptor YWTD-containing repeat homology <YW15>

F:1446-1488/Domain: LDL receptor YWTD-containing repeat homology <YW16>

F:1489-1531/Domain: LDL receptor YWTD-containing repeat homology <YW17>

F:1540-1578/Domain: EGF homology <EG7>

F:1583-1626/Domain: LDL receptor YWTD-containing repeat homology <YW18>

F:1627-1669/Domain: LDL receptor YWTD-containing repeat homology <YW19>

F:1670-1713/Domain: LDL receptor YWTD-containing repeat homology <YW20>

F:1714-1753/Domain: LDL receptor YWTD-containing repeat homology <YW21>

F:1754-1796/Domain: LDL receptor YWTD-containing repeat homology <YW22>

F:1797-1846/Domain: LDL receptor YWTD-containing repeat homology <YW23>

F:1850-1886/Domain: EGF homology <EG8>

F:1934-1976/Domain: LDL receptor YWTD-containing repeat homology <YW24>

F:1977-2019/Domain: LDL receptor YWTD-containing repeat homology <YW25>

F:2020-2063/Domain: LDL receptor YWTD-containing repeat homology <YW26>

F:2064-2105/Domain: LDL receptor YWTD-containing repeat homology <YW27>

F:2106-2151/Domain: LDL receptor YWTD-containing repeat homology <YW28>

F:2159-2241/Domain: EGF homology <EG9>

F:2199-2241/Domain: LDL receptor YWTD-containing repeat homology <YW29>

F:2253-2294/Domain: LDL receptor YWTD-containing repeat homology <YW30>

F:2344-2388/Domain: LDL receptor YWTD-containing repeat homology <YW31>

F:2389-2429/Domain: LDL receptor YWTD-containing repeat homology <YW32>

F:2430-2473/Domain: LDL receptor YWTD-containing repeat homology <YW33>

F:2482-2517/Domain: EGF homology <EG10>

F:2524-2561/Domain: LDL receptor ligand-binding repeat homology <LDL11>

F:2566-2600/Domain: LDL receptor ligand-binding repeat homology <LDL12>

F:2605-2639/Domain: LDL receptor ligand-binding repeat homology <LDL13>

F:2652-2688/Domain: LDL receptor ligand-binding repeat homology <LDL14>

F:2696-2730/Domain: LDL receptor ligand-binding repeat homology <LDL15>

F:2734-2769/Domain: LDL receptor ligand-binding repeat homology <LDL16>

F:2774-2812/Domain: LDL receptor ligand-binding repeat homology <LDL17>

F:2818-2853/Domain: LDL receptor ligand-binding repeat homology <LDL18>

F:2858-2897/Domain: LDL receptor ligand-binding repeat homology <LDL19>

F:2904-2939/Domain: LDL receptor ligand-binding repeat homology <LDL20>

F:2944-2980/Domain: EGF homology <EG11>

F:2986-3021/Domain: EGF homology <EG12>

F:3029-3068/Domain: LDL receptor YWTD-containing repeat homology <YW34>

F:3069-3113/Domain: LDL receptor YWTD-containing repeat homology <YW35>

F:3114-3156/Domain: LDL receptor YWTD-containing repeat homology <YW36>

F:3157-3200/Domain: LDL receptor YWTD-containing repeat homology <YW37>

F:3201-3241/Domain: LDL receptor YWTD-containing repeat homology <YW38>

F:3242-3284/Domain: LDL receptor YWTD-containing repeat homology <YW39>

F:3294-3330/Domain: EGF homology <EG13>

F:3334-3369/Domain: LDL receptor ligand-binding repeat homology <LDL21>

F:3374-3408/Domain: LDL receptor ligand-binding repeat homology <LDL22>

F:3413-3448/Domain: LDL receptor ligand-binding repeat homology <LDL23>

F:3453-3489/Domain: LDL receptor ligand-binding repeat homology <LDL24>

F:3494-3531/Domain: LDL receptor ligand-binding repeat homology <LDL25>

F:3536-3570/Domain: LDL receptor ligand-binding repeat homology <LDL26>

F:3575-3609/Domain: LDL receptor ligand-binding repeat homology <LDL27>

F:3613-3647/Domain: LDL receptor ligand-binding repeat homology <LDL28>

F:3654-3690/Domain: LDL receptor ligand-binding repeat homology <LDL29>

F:3695-3731/Domain: LDL receptor ligand-binding repeat homology <LDL30>

F:3741-3776/Domain: LDL receptor ligand-binding repeat homology <LDL31>

F:3785-3822/Domain: EGF homology <EG14>

F:3828-3860/Domain: EGF homology <EG15>

F:3868-3911/Domain: LDL receptor YWTD-containing repeat homology <YW40>

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 7, 2006, 23:29:32 ; Search time 56.979 Seconds
(without alignments)
4915.754 Million cell updates/sec

Title: US-10-621-855-5
Perfect score: 2131
Sequence: 1 MGLSWSPRPPLMLLVLS.....PRLPILSFLPILLLQLTLW 397

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2131	100.0	397	1	GFR3 MOUSE
2	2058	96.6	385	2	Q92D0 MOUSE
3	1972	92.5	397	2	Q6AXR3 RAT
4	1646.5	77.3	400	1	GFR3 HUMAN
5	1167	54.8	222	2	Q9QZ2 RAT
6	581.5	27.3	465	1	GFR2 CHICK
7	577.5	27.1	444	2	Q792X9 RAT
8	577.5	27.1	464	2	Q5E9X0 BOVIN
9	577.5	27.1	464	2	Q35977 RAT
10	576.5	27.1	463	1	GFR2 MOUSE
11	576.5	27.1	463	2	Q920Y3 MOUSE
12	574.5	27.0	460	2	Q9E29_PONPY
13	574.5	27.0	464	1	GFR2 HUMAN
14	574.5	27.0	464	2	Q6GT9 HUMAN
15	574.5	27.0	464	2	QSRAD6_PONPY
16	564.5	26.5	464	2	QSRAD6_PONPY
17	531	24.9	469	1	GFR1 CHICK
18	519	24.4	495	2	Q75T3 BRARE
19	514.5	24.1	481	2	Q98T78 BRARE
20	513.5	24.1	465	1	GFR1 HUMAN
21	513	24.1	472	2	Q98T79 BRARE
22	510	23.9	463	2	Q35252 MOUSE
23	508.5	23.9	468	1	GFR1 MOUSE
24	508.5	23.9	468	2	Q35246 MOUSE
25	507	23.8	431	2	Q4RG68 TETNG
26	507	23.8	463	2	Q35748 RAT
27	505.5	23.7	468	1	GFR1 RAT
28	490	23.0	431	1	GFR4 CHICK
29	489.5	23.0	484	2	Q4S1R4 TETNG
30	468.5	22.0	333	2	Q4RTG0 TETNG
31	442.5	20.8	358	2	Q922A3 MOUSE

32	436.5	20.5	359	2	Q58J92 HUMAN
33	429.5	20.2	342	2	Q4SDM1 TETNG
34	429	20.1	330	2	Q922A2 MOUSE
35	412	19.3	203	2	Q4SPK7 TETNG
36	375.5	17.6	260	1	GFR4 MOUSE
37	371	17.4	273	1	GFR4 RAT
38	294	13.8	299	1	GFR4 HUMAN
39	294	13.8	299	2	Q5JT74 HUMAN
40	272.5	12.8	247	2	Q4SG83 TETNG
41	264.5	12.4	182	2	Q5JT77 HUMAN
42	232	10.9	394	2	Q6UXV0 HUMAN
43	223.5	10.5	393	2	Q6SUE0 MOUSE
44	204	9.6	225	2	Q9QWK2 MOUSE
45	199.5	9.4	109	2	Q8JG58 AMBME

ALIGNMENTS

RESULT 1

ID	GFR3 MOUSE	STANDARD;	PRT;	397 AA.
AC	Q35118; Q35325; Q55243; Q6NZC2; Q8C8L9;			
DT	25-OCT-2004 (Rel. 45, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DB	GNF family receptor alpha 3 precursor (GFR-alpha 3) (GFRalpha3).			
GN	Name=Gfr3;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muridea; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=C57BL/6; TISSUE=Heart;			
RC	MEDLINE=98205811; PubMed=9535755; DOI=10.1006/bbrc.1998.8361;			
RA	Tomoto S., Ito S., Yang L.-X., Kiuchi K.;			
RT	Molecular cloning and expression analysis of GFR alpha-3, a novel			
RT	cDNA related to GDNFR alpha and NTNR-alpha.			
RL	Biochem. Biophys. Res. Commun. 244:849-853 (1998).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	MEDLINE=98420233; PubMed=9749804;			
RA	Widenfalk J., Tomac A., Lindqvist E., Hoffer B., Olson L.;			
RT	"GFR-alpha-3, a protein related to GFRalpha-1, is expressed in			
RT	developing peripheral neurons and ensheathing cells."			
RL	Eur. J. Neurosci. 10:1508-1517 (1998).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RC	PubMed=9448325; DOI=10.1073/pnas.95.3.1295;			
RA	Naveilhan P., Baudet C., Mikaela A., Shen L., Westphal H., Ernfor P.;			
RT	Expression and regulation of GFRalpha3, a glial cell line-derived			
RT	neurotrophic factor family receptor."			
RL	Proc. Natl. Acad. Sci. U.S.A. 95:1295-1300 (1998).			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE.			
RC	MEDLINE=98245162; PubMed=9576965; DOI=10.1073/pnas.95.10.5801;			
RA	Balgh R.H., Gorodinsky A., Golden J.P., Tansey M.G., Keck C.L.,			
RA	Popescu N.C., Johnson E.M. Jr., Milbrandt J.;			
RT	"GFRalpha3 is an orphan member of the GDNF/neurturin/persephin			
RT	receptor family."			
RL	Proc. Natl. Acad. Sci. U.S.A. 95:5801-5806 (1998).			
RN	[5]			
RP	NUCLEOTIDE SEQUENCE.			
RC	MEDLINE=98271460; PubMed=9608533; DOI=10.1006/mcne.1998.0667;			
RA	Trupp M., Raynoschek C., Belluardo N., Ibanez C.F.;			
RT	"Multiple GFR1-anchored receptors control GDNF-dependent and			
RT	independent activation of the c-Ret receptor tyrosine kinase."			
RL	Mol. Cell. Neurosci. 11:47-63 (1998).			
RN	[6]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].			
RC	STRAIN=C57BL/6J; TISSUE=Adrenal gland;			

RX MEDLINE=22354683; PubMed=12468951; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusica V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltala L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shindala K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Waki J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 RN [7]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny K.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!- FUNCTION: Receptor for the glial cell line-derived neurotrophic
 CC factor, artemin. Mediates the artemin-induced autophosphorylation
 CC and activation of the RET receptor tyrosine kinase (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the GDNFR family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; AB008833; BAA23562.1; -; mRNA.
 CC EMBL; AF041842; AAC23558.1; -; mRNA.
 CC EMBL; AF036163; AAC24468.1; -; mRNA.
 CC EMBL; AF051766; AAC24354.1; -; mRNA.
 CC EMBL; AF020305; AAB70931.1; -; mRNA.

DR EMBL; AK046542; BAC32778.1; -; mRNA.
 DR EMBL; BC066202; AAH66202.1; -; mRNA.
 DR PIR; JE0082; JE0082.
 DR Ensembl; ENSMUSG00000024366; Mus musculus.
 DR MGI; MGI:1201403; Gfra3.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0008046; F:axon guidance receptor activity; IMP.
 DR GO; GO:0015026; F:coreceptor activity; TAS.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007411; F:axon guidance; IMP.
 DR GO; GO:0007422; P:peripheral nervous system development; IMP.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; TAS.
 DR InterPro; IPR003438; GDNF_receptor.
 DR InterPro; IPR003505; GDNF_receptorA3.
 DR PANTHER; PTHR10269; GDNF_receptor; 1.
 DR Pfam; PF02351; GDNF; 1.
 DR PRINTS; PR01319; GDNFRALPHA3.
 DR PRINTS; PR01316; GDNFRCEPTOR.
 DR Glycoprotein; GPI-anchor; Membrane; Receptor; Signal.
 DR SIGNAL 1 28 Potential.
 FT CHAIN 29 371 GDNF family receptor alpha 3.
 FT PROPEP 372 397 Removed in mature form (potential).
 FT LIPID 371 371 GPI-anchor amidated asparagine (potential).
 FT CARBOHYD 92 92 N-linked (GlcNAc. .) (potential).
 FT CARBOHYD 145 145 N-linked (GlcNAc. .) (potential).
 FT CARBOHYD 306 306 N-linked (GlcNAc. .) (potential).
 FT CONFLICT 5 6 WS -> LE (in Ref. 2 and 3).
 FT CONFLICT 66 66 S -> C (in Ref. 6).
 FT CONFLICT 218 218 A -> P (in Ref. 2, 3 and 5).
 FT CONFLICT 314 314 T -> S (in Ref. 7).
 SQ SEQUENCE 397 AA; 44307 MW; BB66CEFF65D32A4B9 CRC64;
 Query Match 100.0%; Score 2131; DB 1; Length 397;
 Best Local Similarity 100.0%; Pred. No. 3.7e-171;
 Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGLSWSPRPPLMLILLVLSLWLPGLGAGNSLATENRFVNSCTQARKKEANPACKAAAYQH 60
 DB 1 MGLSWSPRPPLMLILLVLSLWLPGLGAGNSLATENRFVNSCTQARKKEANPACKAAAYQH 60
 QY 61 LGSCTSSLSRPLPEESAMSDCLEAAEAFOLRNSSLIDCRCHRRMKHQATCLDIYVTVHPA 120
 DB 61 LGSCTSSLSRPLPEESAMSDCLEAAEAFOLRNSSLIDCRCHRRMKHQATCLDIYVTVHPA 120
 QY 121 RSLGDYELDVSPYEDTVTSKPWNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180
 DB 121 RSLGDYELDVSPYEDTVTSKPWNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180
 QY 181 BACSGIRCORHLCLALQALRSFFKEAASHAQGLLCPAPEDAGCGERRNTIAPSCALPS 240
 DB 181 BACSGIRCORHLCLALQALRSFFKEAASHAQGLLCPAPEDAGCGERRNTIAPSCALPS 240
 QY 241 VTPNCLDLSRCRADPLCLRSRLMDPFTQCHPMDILGTCTAQSCRLRAYLGLGTAMTPN 300
 DB 241 VTPNCLDLSRCRADPLCLRSRLMDPFTQCHPMDILGTCTAQSCRLRAYLGLGTAMTPN 300
 QY 301 FISKVNTTVALSCTCRSGNQLQDECEQLERSFSQNPCLVEIAAKMRPHRLQFSQDWADS 360
 DB 301 FISKVNTTVALSCTCRSGNQLQDECEQLERSFSQNPCLVEIAAKMRPHRLQFSQDWADS 360
 QY 361 TFSVVQQQNSPALRLQPRLPILSFIPLILLQTLW 397
 DB 361 TFSVVQQQNSPALRLQPRLPILSFIPLILLQTLW 397
 RESULT 2
 Q9R2D0_MOUSE PRELIMINARY; PRT; 385 AA.
 ID Q9R2D0_MOUSE
 AC Q9R2D0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE TGF-beta-related neurotrophic receptor-3 precursor.
GN Name=Gfra3; Synonyms=TrnR-3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Swiss-Webster /NIH; TISSUE=Embryo;
RA Zhong J., Annie M., Tolle A., Heumann R.;
RT "Molecular cloning of a new member of TrnR family.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y15110; CAA75384.1; -; mRNA.
DR MGI; MGI:1201403; Gfra3.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0008046; F:axon guidance receptor activity; IMP.
DR GO; GO:0015036; F:coreceptor activity; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007411; P:axon guidance; IMP.
DR GO; GO:0007422; P:peripheral nervous system development; IMP.
DR GO; GO:007169; P:transmembrane receptor protein tyrosine kin. .; TAS.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003505; GDNF_receptorA3.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01319; GDNFRALPHA3.
DR PRINTS; PR01316; GDNFRECEPTOR.
KW Receptor; Signal.
FT SIGNAL 1 15 Potential.
SQ SEQUENCE 385 AA; 42997 MW; 91A7F3F9FF30ED14 CRC64;

Query Match 96.6%; Score 2058; DB 2; Length 385;
Best Local Similarity 99.7%; Pred. No. 5.2e-165;
Matches 384; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 MILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSGTSSLSRPL 72
Db 1 MILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSGTSSLSRPL 60
Qy 73 PLESAASADCLEAAEQRLNSLLDCRCHRRMKHQATCLDIYTVHPARSIGDYELDVSP 132
Db 61 PLESAASADCLEAAEQRLNSLLDCRCHRRMKHQATCLDIYTVHPARSIGDYELDVSP 120
Qy 133 YEDTVTSKPWKNSLKLNLKPSDCLKFKFAMLTCLHDKCDRLRKAYGACSGIRCORHL 192
Db 121 YEDTVTSKPWKNSLKLNLKPSDCLKFKFAMLTCLHDKCDRLRKAYGACSGIRCORHL 180
Qy 193 CLAQLRFFFEKAESHAQGLLLCPAPEDAGCGRRRNTIAPSCALPSVTPNCLDLRSFC 252
Db 181 CLAQLRFFFEKAESHAQGLLLCPAPEDAGCGRRRNTIAPSCALPSVTPNCLDLRSFC 240
Qy 253 RADPLCRSLRMDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAMTNFISKVNTTVALS 312
Db 241 RADPLCRSLRMDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAMTNFISKVNTTVALS 300
Qy 313 CTCRGSGLNDECEQLERSFSONPCLVEAIAAKMRFHQQLPSQDADSTTSVWQQNSNP 372
Db 301 CTCRGSGLNDECEQLERSFSONPCLVEAIAAKMRFHQQLPSQDADSTTSVWQQNSNP 360
Qy 373 ALRLQPLPILSILPILLQTLW 397
Db 361 ALRLQPLPILSILPILLQTLW 385

RESULT 3
Q6AXR3 RAT PRELIMINARY; PRT; 397 AA.
AC Q6AXR3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Gial cell line derived neurotrophic factor family receptor alpha
DE 3.

GN Name=Gfra3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullay S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RG NIH MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC079378; AAH79378.1; -; mRNA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003505; GDNF_receptorA3.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01319; GDNFRALPHA3.
DR PRINTS; PR01316; GDNFRECEPTOR.
KW Receptor.
SQ SEQUENCE 397 AA; 44053 MW; E11D2E7B9CB46AF8 CRC64;

Query Match 92.5%; Score 1972; DB 2; Length 397;
Best Local Similarity 92.9%; Pred. No. 9.6e-158;
Matches 369; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MGLSWSPPRLMLLLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60
Db 1 MGLSWSPPRLMLLLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60
Qy 61 LGSCTSSLSRPLPLEBSAMSADCLEAAEQRLNSLLDCRCHRRMKHQATCLDIYTVHPA 120
Db 61 LGSCTSSLSRPLPLEBSAMSADCLEAAEQRLNSLLDCRCHRRMKHQATCLDIYTVHPV 120
Qy 121 RSLGDIYELDVSPYEDTVTSKPWKNSLKLNLKPSDCLKFKFAMLTCLHDKCDRLRKAYG 180
Db 121 RSLGDIYELDVSPYEDTVTSKPWKNSLKLNLKPSDCLKFKFAMLTCLHDKCDRLRKAYG 180
Qy 181 EACSGIRCORHLCAQLRFFFEKAESHAQGLLLCPAPEDAGCGRRRNTIAPSCALPS 240
Db 181 EACSGIRCORHLCAQLRFFFEKAESHAQGLLLCPAPEDAGCGRRRNTIAPSCALPS 240
Qy 241 VTPNCLDLRSFCRADPLCRSLRMDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAMTN 300
Db 241 VAPNCLDLRSFCRADPLCRSLRMDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAMTN 300
Qy 301 FISKVNTTVALSCTCRGSGLNDECEQLERSFSONPCLVEAIAAKMRFHQQLPSQDADST 360
Db 301 FISKVNTTVALSCTCRGSGLNDECEQLERSFSONPCLVEAIAAKMRFHQQLPSQDADST 360

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QY 361 TFSVVOQNSPALRLOPLRPLTSLPSILPLILLOTLW 397
DB 361 TFSVVOQNSPALRPLRPLTSLPSILPLILLOTLW 397

RESULT 4
GPR3 HUMAN
ID GPR3_HUMAN STANDARD; PRT; 400 AA.
AC O60609; Q60W20; Q8IU22;
DT 16-OCT-2001 (Rel. 40, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DE GDNF family receptor alpha 3 precursor (GPR-alpha 3) (GPRalpha3).
GN Name=GPR3; ORFNames=UNQ339/PRO538/PRO3664;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND TISSUE SPECIFICITY.
RX MEDLINE=98245162; PubMed=9576965; DOI=10.1073/pnas.95.10.5801;
RA Baloh R.H., Gorodinsky A., Golden J.P., Tansey M.G., Keck C.L.,
RA Popescu N.C., Johnson E.M. Jr., Milbrandt J.;
RA "GPRalpha3 is an orphan member of the GDNF/neurturin/persephin
RT receptor family.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:5801-5806 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).
RX MEDLINE=22687296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wiand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RA "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270 (2003).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallahy S.J.,
RA Bosak S.A., McWeeney P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP PROTEIN SEQUENCE OF 32-46.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
```

Protein Sci. 13:2819-2824 (2004).

[5]

FUNCTION.

RA Baloh R.H., Tansey M.G., Lampe P.A., Fahrner T.J., Enomoto H.,
RA Simburger K.S., Leitner M.L., Araki T., Johnson E.M. Jr.,
RA Milbrandt J.;
RT "Artemin, a novel member of the GDNF ligand family, supports
RT peripheral and central neurons and signals through the GPRalpha3-RET
RT receptor complex.";
RL Neuron 21:1291-1302 (1998).

CC -!- FUNCTION: Receptor for the glial cell line-derived neurotrophic
CC factor, artemin. Mediates the artemin-induced autophosphorylation
CC and activation of the RET receptor tyrosine kinase. Moderate
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O60609-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O60609-2; Sequence=VSP_010942;
CC -!- TISSUE SPECIFICITY: Widely expressed in adult and fetus which
CC exhibit a similar pattern. Essentially not expressed in the
CC central nervous system, but highly expressed in several sensory
CC and sympathetic ganglia of the peripheral nervous system. Moderate
CC expression in many nonneural tissues, particularly those of the
CC digestive and urogenital systems, but high expression in stomach
CC and appendix. Several types of glandular tissues show low
CC expression. Very low or no expression detected in the
CC hematopoietic system.
CC -!- SIMILARITY: Belongs to the GDNFR family.

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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

DR EMBL; AF051767; AAC24355.1; -; mRNA.
DR EMBL; AY358997; AAQ89356.1; -; mRNA.
DR EMBL; AY359037; AAQ89396.1; -; mRNA.
DR EMBL; BC037951; AAH37951.1; -; mRNA.
DR Ensembl; ENSG00000146013; Homo sapiens.
DR HGNC; HGNC:4245; GPR3.
DR MIM; 605710; -.
DR GO; GO:0019898; C:extrinsic to membrane; TAS.
DR GO; GO:0005102; F:receptor binding; TAS.
DR GO; GO:0007422; P:peripheral nervous system development; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003505; GDNF_receptorA3.
DR PANTHER; PTHR10269; GDNF_receptor; 1.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01319; GDNFRALPHA3.
DR PRINTS; PR01316; GDNFRCEPTOR.
KW Alternative splicing; Direct protein sequencing; Glycoprotein;
KW GPI-anchor; Lipoprotein; Membrane; Receptor; Signal.
FT SIGNAL 1 31
FT CHAIN 32 374 GDNF family receptor alpha 3.
FT PROPEP 375 400 Removed in mature form (potential).
FT LIPID 374 374 GPI-anchor amidated asparagine
(potential).
FT CARBOHYD 95 95 N-linked (GlcNAc...) (potential).
FT CARBOHYD 148 148 N-linked (GlcNAc...) (potential).
FT CARBOHYD 309 309 N-linked (GlcNAc...) (potential).
FT VARSPLIC 127 157 Missing (in isoform 2).
FT CONFLICT 108 108 K -> R (in Ref. 1).
FT SEQUENCE 400 AA; 44511 MW; B0BC252FE1F072C7 CRC64;
SQ

Query Match 77.3%; Score 1646.5; DB 1; Length 400;
Best Local Similarity 77.8%; Pred. No. 2.7e-130;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

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OY 7 PRPP-LLMILLVLSLWPLGAGNSLATENRFVNSCTQARKCEANPACKAAYQHLGSC 65
Db 9 PLPPVVLMLLLPLPSPLAAGDPLPTESRLMNSCLQARRKQADPTCSAAYHLDSC 68
OY 66 SLSRPLPLESAMSADCLAEAEQLRNSLIDCRCHRMKQATCLDIYTWVHPARSLGD 125
Db 69 SSIISPLSEEPSVADCLAEAAQQQLNSLIGCMCHRMKQVACLDIYTWVHRRARSLG 128
OY 126 YELDVSPYEDVTSPKWNLSKLNKLPDSDCLCKFAMLCITLHDKCDRLRKAYGEACSG 185
Db 129 YELDVSPYEDVTSPKWNLSKLNKLPDSDCLCKFAMLCITLHDKCDRLRKAYGEACSG 188
OY 186 IRCQHLCLAQLRFFFEKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPSVTPNC 245
Db 189 PHCQRHVCLRLQLTFEFAAEPAHQGLLLCPAPNDRCGGERNTIAPNCALPPVAPNC 248
OY 246 LDLRSFCRADPLCRSLMDFTQCHPMDILGTCAEQSRCLRAYLGLGTAMTNFISKV 305
Db 249 LELRLCFSDPLCRSLMDFTQCHPMDILGTCAEQSRCLRAYLGLGTAMTNFISGV 308
OY 306 NTTVALSCTCRSGNLQDECEQLERSFSONPCLVEAIAAKRFRHQLFSQDWDSTFVW 365
Db 309 NTSVALSCTCRSGNLQDECEMLEGFFSHNPCLTEAIAAKRFRHQLFSQDWDSTFVW 368
OY 366 QQNSNPALRQPLRPLISFSLPILLLQTLW 397
Db 369 AHQENPAVRPQWPVPSLFSCTPLPLILLSLW 400
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RESULT 5

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OYQZG2 RAT
ID Q90ZG2 RAT PRELIMINARY; PRT; 222 AA.
AC Q90ZG2;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE GDNF-family receptor alpha 3 (Fragment).
GN Name=Gfra3; Synonyms=GFRalpha-3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Cochlea;
RX MEDLINE=20185640; PubMed=10719212; DOI=10.1016/S0169-328X(99)00328-9;
RA Stover T., Gong T.L., Cho Y., Altschuler R.A., Lomax M.I.;
RT "Expression of the GDNF family members and their receptors in the
RT mature rat cochlea.";
RL Brain Res. Mol. Brain Res. 76:25-35 (2000).
DR EMBL; AF184920; AAF01242.1; -; mRNA.
DR Ensembl; ENSRNORG0000020309; Rattus norvegicus.
DR RGD; 620502; Gfra3.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003505; GDNF_receptorA3.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01319; GDNFRALPHA3.
DR PRINTS; PR01316; GDNFRECEPTOR.
KW Receptor.
FT NON_TER 1
FT NON_TER 222
FT NON_TER 222
SQ SEQUENCE 222 AA; 24791 MW; A9610F6462468C74 CRC64;
Query Match 54.8%; Score 1167; DB 2; Length 222;
Best Local Similarity 96.4%; Pred. No. 3.8e-90;
Matches 214; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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OY 136 TVTSKPWNLSKLNKLPDSDCLCKFAMLCITLHDKCDRLRKAYGEACSGRCORHLCLA 195
Db 1 TVTSKPWNLSKLNKLPDSDCLCKFAMLCITLHDKCDRLRKAYGEACSGRCORHLCLA 60
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OY 196 QLRFFFEKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPSVTPNCILDRSFCRAD 255
Db 61 QLRFFFEKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPSVTPNCILDRSFCRAD 120
OY 256 PLCSRLMDFTQCHPMDILGTCAEQSRCLRAYLGLGTAMTNFISKVTVALSCTC 315
Db 121 PLCSRLMDFTQCHPMDILGTCAEQSRCLRAYLGLGTAMTNFISKVTVALSCTC 180
OY 316 RSGNLQDECEQLERSFSONPCLVEAIAAKRFRHQLFSQDW 357
Db 181 RSGNLQDECEQLERSFSONPCLVEAIAAKRFRHQLFSQDW 222
```

RESULT 6

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ID GFRA2 CHICK STANDARD; PRT; 465 AA.
AC O13157;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE GDNF family receptor alpha 2 precursor (GFR-alpha 2) (Neurturin
DE receptor alpha) (NTRN-alpha) (NTRN-alpha) (GDNF receptor beta)
DE (GDNFR-beta).
GN Name=GFRA2; Synonyms=GDNFRB;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=97336104; PubMed=9192899; DOI=10.1038/42729;
RA Buj-Bello A., Adu J., Pinon L.G.P., Horton A., Thompson J.,
RA Rosenthal A., Chinchetru M., Buchman V.L., Davies A.M.;
RT "Neurturin responsiveness requires a GPI-linked receptor and the Ret
RT receptor tyrosine kinase.";
RL Nature 387:721-724 (1997).
CC -!- FUNCTION: Receptor for neurturin. Mediates the NRTN-induced
CC autophosphorylation and activation of the RET receptor. Also able
CC to mediate GDNF signaling through the RET tyrosine kinase receptor
CC (by similarity).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- SIMILARITY: Belongs to the GDNF family.
CC
```

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DR EMBL; U90542; AAB61571.1; -; mRNA.
DR Ensembl; ENSGALG0000001795; Gallus gallus.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003504; GDNF_receptorA2.
DR PANTHER; PTHR10269; GDNF_receptor; 1.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01318; GDNFRALPHA2.
DR PRINTS; PR01316; GDNFRECEPTOR.
KW Glycoprotein; GPI-anchor; Lipoprotein; Membrane; Receptor; Signal.
FT SIGNAL 1 21
FT CHAIN 22 445
FT PROPEP 446 465
FT LIPID 446 445
FT CARBOHYD 355 355
FT CARBOHYD 387 387
FT CARBOHYD 412 412
SQ SEQUENCE 465 AA; 51909 MW; 22CD9024ED971F06 CRC64;
Query Match 27.3%; Score 581.5; DB 1; Length 465;
Best Local Similarity 36.0%; Pred. No. 2.1e-40;
Matches 130; Conservative 51; Mismatches 135; Indels 45; Gaps 11;
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